10/587,372

(51) International Patent Classification 5 : C12N 15/82, 15/84, A01H 5/00	A2	(11) International Publication Number: **WO 94/28146** (43) International Publication Date: 8 December 1994 (08.12.94)

(21) International Application Number: PCT/EP94/01671

(22) International Filing Date: 20 May 1994 (20.05.94)

(30) Priority Data:
P 43 17 596.1   24 May 1993 (24.05.93)   DE

(71) Applicant (for all designated States except US): HOECHST SCHERING AGREVO GMBH [DE/DE]; Gerichtstrasse 27, D-13347 Berlin (DE).

(72) Inventors; and
(75) Inventors/Applicants (for US only): HESSE, Holger [DE/DE]; Brundhildstrasse 9, D-10829 Berlin (DE). MÜLLER-RÖBER, Bernd [DE/DE]; Siemensstrasse 71, D-12247 Berlin (DE).

(81) Designated States: CA, HU, JP, RU, UA, US, European patent (AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE).

Published
Without international search report and to be republished upon receipt of that report.

(54) Title: DNA SEQUENCES AND PLASMIDS FOR THE PREPARATION OF SUGAR BEET WITH CHANGED SUCROSE CONCENTRATION

(57) Abstract

DNA sequences and plasmids are described, that by integration in a plant genome of sugar beet change the sucrose concentration, as well as transgenic plants that by introduction of the DNA sequences of the invention causes changes in sugar concentration.

Title: DNA sequences and plasmids for the preparation of
sugar beet with changed sucrose concentration

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Field of the invention
The present invention relates to DNA sequences and
plasmids, containing these DNA sequences, which by
integration into the genome of a sugar-beet plant, changes
10   the sugar metabolism of the plant to be changed. The
invention also relates to transgenic plants formed with
the help of these sequences.

Sucrose is of central importance for the plant and serves
15   many functions. For the long distance transport of
photoassimilates and/or energy between various organs in
plants, sucrose is almost exclusively used. The sucrose,
which is transported in a specific heterotrophic organ,
determines the growth and the development of this organ.
20   Thus it is known, e.g. from EP 442 592, that transgenic
plants, in which the transport away of the sucrose from
the exporting leaves is inhibited by expression of an
apoplastic invertase, shows a strong reduction in the
growth of e.g. roots or tubers in the case of potato
25   plants. For tobacco plants, the principal importance of
sucrose as the central function for the long distance
transport of energy carriers within the plant is described
(von Schaewen et al, 1990, EMBO J 9: 3033-3044).

30   Further it is also known from EP 455 316 that DNA
sequences present on plasmids, after introduction in a
plant genome of a potato plant can affect the starch
biosynthesis as well altering the amount and composition
of the protein in the potato tubers.

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Whilst it has known that a reduction of the amount of
sucrose imported in the heterotrophic organs, such as
tubers and seeds, leads to loss of yield, it is not known
whether an increase in the amount of sucrose in the
5   photosynthetically active parts of the plant, mainly the
leaves, leads to a better supply of heterotrophic organs
and thus to an increase in yield.

Besides sucrose and/or the hexoses, glucose and fructose,
10 derived from sucrose, have the property of protection of
plants against frost damage at low temperatures. Frost
damage is one of the main limiting factors in agricultural
productivity in the northern hemisphere. Temperatures
below freezing lead to the formation of ice crystals.
15 Since the growing ice crystals consist of pure water,
water is abstracted from the cells as the temperature
falls.

This dehydration has at least two potential damaging
20 results:
    1.   All dissolved substances within a cell are strongly
         concentrated and the cell contracts following the
         loss of water. Highly concentrated salts and organic
         acids lead to membrane damage.
25

    2.   With rehydration from dew, the previously contacted
         cells reexpand. The cell membrane also expands
         again. The volume expansion puts a heavy mechanical
         load on the membrane.
30

It is thus clear that a freezing/dew cycle can lead to
severe membrane damage of the cells and thus to damage to
the plant.

35 It thus appears worth trying to hinder the freezing. One

3

possible strategy is the increased formation of
osmotically active substances in the cytosol of plant
cells. This should lead to a lowering of the freezing
point. Osmotically active substances include sucrose
5   and/or the two hexoses derived from sucrose.

The increased formation of sucrose and/or the two hexoses
at low temperatures is desirable in the growing plant.
Another situation can exist in the harvested parts of a
10   plant, especially in storage.

In relation to the economic aspects, sucrose thus
possesses two especially important functions:
1   as the transport form for the distant transport of
15   photoassimilates,
2   as an osmotically active substance with the
            desirable activity of lowering the freezing point in
            intact, growing plants.

20   The biosynthesis pathways for the formation of sucrose,
either from the primary photosynthesis products (in the
leaf) or by breakdown of starch (in the storage organs
e.g. of potatoes), are known.

25   It is however, not known how and in what way changes of
the carbohydrate concentration in sugar beet can be
achieved since it is not possible to use even very similar
genes such as for example genes that code for a sucrose
synthase, ADP-glucose pyrophosphorylase or sucrose
30   phosphate synthase of the potato with satisfactory success
for the preparation of sugar beet with changed sucrose
concentration. An exact analysis and determination of the
DNA sequences or sequence fragments for the sugar beet is
thus required.

35

4

To change the sugar concentration in sugar beet, DNA
sequences are now provided which code for the small and
large subunit of the ADP glucose pyrophosphorylase, the
sucrose synthase and the sucrose phosphate synthase of
5   sugar beet (Seq. ID No 1-4).

These DNA sequences can be introduced into plasmids and in
this way combined with steering elements for expression in
eukaryotic cells. Such steering elements are on the one
10   hand transcription promoters and on the other hand
transcription terminators. Each plasmid comprises:

    a)   a suitable promoter which ensures that the coding
          sequence meets a suitable time point or in the
15   specified developments in the transgenic plant or in
          determined genes of transgenic plants;

    b)   at least a coding sequence for sugar beet that
          i)   is so coupled to the promoter that the
20   formation of an RNA is allowed which is into a
                protein, whereby the protein demonstrates an
                enzymatic activity which leads to a change of
                the sucrose concentration in the plant, or
          ii)   which is so coupled to the promoter that the
25   coding part is read, which leads to the
                formation of a so-called anti-sense RNA which
                under-expresses the formation of the protein
                coded from an endogenous gene in the plant,
                that is involved in the sucrose biosynthesis;
30   and

    c)   A non-coding termination sequence that contains the
          signal for the termination and polyadenylation of
          the transcript.

35

5

The coding sequences named under b) are the sequences that code for the large and small subunit of the ADP glucose pyrophosphorylase, for the sucrose phosphate synthase and for the sucrose synthase of sugar beet.

5   The large subunit of the ADP-glucose-pyrophosphorylase has the following nucleotide sequence (Seq. ID No. 1):

CAAAAGAAAA ACTTCCCATT TCTACTTCTT TGCACAATAT AATTTCCCAC   0050

CAATTTTTCT TTAAATTTCT CACTTTCATT TAATCAGTTT TCAGCAACAT   0100

TCTGATACTC GACAACCCAC TTTCTGTTCT CCCAAGATTC CAAACCTCTG   0150

ATTCTCATTC CACTAATATT TTTGCTTATT TTTTTCTGG ATTTAAAGAA   0200

AAGCT ATG GAT GCA AGT GCA GCA GCC ATA AAT GTC AAT GCC CAT   0243
      Met Asp Ala Ser Ala Ala Ala Ile Asn Val Asn Ala His
                        5   10

TTA ACA GAA GTT GGA AAG AAA CGT TTT TTA GGA GAG AGA ATC AGT 0288
Leu Thr Glu Val Gly Lys Lys Arg Phe Leu Gly Glu Arg Ile Ser
    15   20   25

CAA AGT TTG AAG GGT AAA GAT CTG AGA GCT CTG TTT TCA AGA ACT 0333
Gln Ser Leu Lys Gly Lys Asp Leu Arg Ala Leu Phe Ser Arg Thr
    30   35   40

GAG AGC AAG GGT AGA AAT GTC AAT AAA CCT GGG GTT GCA TTT TCT 0378
Glu Ser Lys Gly Arg Asn Val Asn Lys Pro Gly Val Ala Phe Ser
    45   50   55

GTT CTC ACC TCA GAT TTT AAT CAA AGT GTT AAA GAA TCT TTG AAA 0423
Val Leu Thr Ser Asp Phe Asn Gln Ser Val Lys Glu Ser Leu Lys
    60   65   70

6

```
TAT GAG CCA GCA TTA TTT GAA TCT CCA AAA GCT GAC CCA AAA AAT   0468
Tyr Glu Pro Ala Leu Phe Glu Ser Pro Lys Ala Asp Pro Lys Asn
    75              80              85


GTG GCT GCA ATT GTG CTG GGT GGT GGT GCT GGG ACT CGC CTC TTT   0513
Val Ala Ala Ile Val Leu Gly Gly Gly Ala Gly Thr Arg Leu Phe
    90              95              100


CCT CTT ACT AGC AGG AGA GCT AAG CCA GCA GTG CCA ATT GGA GGG   0558
Pro Leu Thr Ser Arg Arg Ala Lys Pro Ala Val Pro Ile Gly Gly
    105             110             115


TGT TAC AGG CTG ATT GAT GTG CCT ATG AGC AAC TGC ATC AAC AGT   0603
Cys Tyr Arg Leu Ile Asp Val Pro Met Ser Asn Cys Ile Asn Ser
    120             125             130


GGC ATT AGA AAG ATT TTC ATT CTT ACC CAG TTC AAT TCG TTT TCG   0648
Gly Ile Arg Lys Ile Phe Ile Leu Thr Gln Phe Asn Ser Phe Ser
    135             140             145


CTT AAT CGT CAT CTT GCT CGA ACC TAT AAT TTT GGA GAT GGT GTG   0693
Leu Asn Arg His Leu Ala Arg Thr Tyr Asn Phe Gly Asp Gly Val
    150             155             160


AAT TTT GGG GAT GGC TTT GTG GAG GTT TTT GCT GCT ACA CAA ACA   0738
Asn Phe Gly Asp Gly Phe Val Glu Val Phe Ala Ala Thr Gln Thr
    165             170             175
```

7

```
CCT GGA GAA TCA GGA AAG AAA TGG TTC CAG GGC ACC GCT GAT GCA   0783
Pro Gly Glu Ser Gly Lys Lys Trp Phe Gln Gly Thr Ala Asp Ala
    180                 185                 190


GTA AGA CAG TTT TTC TGG GCA TTT GAG GAT TCC AAA TCC AAG GAT   0828
Val Arg Gln Phe Phe Trp Ala Phe Glu Asp Ser Lys Ser Lys Asp
    195                 200                 205


GTC GAG CAT ATA GTT ATT TTA TCC GGT GAT CAT CTT TAC CGA ATG   0873
Val Glu His Ile Val Ile Leu Ser Gly Asp His Leu Tyr Arg Met
    210                 215                 220


GAT TAC ATG AGT TTT TGG CAG AAG CAC ATT GAC ACC AAT GCT GAT   0918
Asp Tyr Met Ser Phe Trp Gln Lys His Ile Asp Thr Asn Ala Asp
    225                 230                 235


ATT ACA GTG TCA TGC ATA CCC ATG GAT GAC AGC CGT GCA TCG GAT   0963
Ile Thr Val Ser Cys Ile Pro Met Asp Asp Ser Arg Ala Ser Asp
    240                 245                 250


TAT GGG CTG ATG AAG ATT GAT CAC ACT GGA CGC ATT GTC CAT TTT   1008
Tyr Gly Leu Met Lys Ile Asp His Thr Gly Arg Ile Val His Phe
    255                 260                 265


GCA GAA AAA CCC AAG GGT TCT GAT CTA ACA GCA ATG CAA GTA GAT   1053
Ala Glu Lys Pro Lys Gly Ser Asp Leu Thr Ala Met Gln Val Asp
    270                 275                 280
```

8

ACA ACT GTT CTT GGG CTC TCT GAC CTT GAA GCT ATG TCA AAT CCA   1098
Thr Thr Val Leu Gly Leu Ser Asp Leu Glu Ala Met Ser Asn Pro
    285   290   295

TAT ATT GCA TCA ATG GGT GTT TAT GTC TTT CGA ACG GAT GTT CTT   1143
Tyr Ile Ala Ser Met Gly Val Tyr Val Phe Arg Thr Asp Val Leu
    300   305   310

ATG GAG CTT CTC AAT CGA AAA TAC CCT TCA AGC AAT GAT TTT GGC   1188
Met Glu Leu Leu Asn Arg Lys Tyr Pro Ser Ser Asn Asp Phe Gly
    315   320   325

TCT GAG ATT ATT CCT TCA GCT GTA GGA GAG TCT AAT GTT CAG GCA   1233
Ser Glu Ile Ile Pro Ser Ala Val Gly Glu Ser Asn Val Gln Ala
    330   335   340

TAT CTA TTT AAT GAC TAC TGG GAG GAT ATC GGA ACC ATA AAG TCT   1278
Tyr Leu Phe Asn Asp Tyr Trp Glu Asp Ile Gly Thr Ile Lys Ser
    345   350   355

TTC TTT GAT TCC AAT TTG GCC CTT ACA CAA CAG CCT CCC AAG TTT   1323
Phe Phe Asp Ser Asn Leu Ala Leu Thr Gln Gln Pro Pro Lys Phe
    360   365   370

GAA TTC TAC GAT CCA AAA ACA CCT TTT TAT ACA TCT GCA AGA TTT   1368
Glu Phe Tyr Asp Pro Lys Thr Pro Phe Tyr Thr Ser Ala Arg Phe
    375   380   385

9

```
CTG CCT CCT ACA AAA GTC GAC AGG TGC AAG ATT GTC GAT TCC ATT   1413
Leu Pro Pro Thr Lys Val Asp Arg Cys Lys Ile Val Asp Ser Ile
    390               395               400


GTA TCC CAT GGT TGT TTT CTA CAG GAG TCT AGC ATC CAA CAT TCC   1458
Val Ser His Gly Cys Phe Leu Gln Glu Ser Ser Ile Gln His Ser
    405               410               415


ATT GTT GGT GTT CGC TCA AGA TTA GAG TCC GGG GTT GAG TTC CAG   1503
Ile Val Gly Val Arg Ser Arg Leu Glu Ser Gly Val Glu Phe Gln
    420               425               430


GAC ACC ATG ATG ATG GGC GCA GAT TAC TAT CAA ACT GAA TCA GAA   1548
Asp Thr Met Met Met Gly Ala Asp Tyr Tyr Gln Thr Glu Ser Glu
    435               440               445


ATT GCT TCT CTG CTT GCT GAG GGA AAG GTT CCT GTT GGT GTC GGA   1593
Ile Ala Ser Leu Leu Ala Glu Gly Lys Val Pro Val Gly Val Gly
    450               455               460


CAG AAT ACC AAA ATA AAG AAT TGC ATA ATT GAC AAG AAC GCC AAA   1638
Gln Asn Thr Lys Ile Lys Asn Cys Ile Ile Asp Lys Asn Ala Lys
    465               470               475


ATT GGA AAA GAT GTG GTA ATC GCA AAC ACG GAT GGT GTT GAG GAA   1683
Ile Gly Lys Asp Val Val Ile Ala Asn Thr Asp Gly Val Glu Glu
    480               485               490
```

10

```
GCA GAT AGA CCA AAT GAA GGC TTT TAC ATC AGG TCG GGC ATT ACC   1728
Ala Asp Arg Pro Asn Glu Gly Phe Tyr Ile Arg Ser Gly Ile Thr
    495             500             505
```

```
ATC ATT TTG AAG AAC GCA ACC ATA CAA GAC GGT CTT GTG ATT TAG   1773
Ile Ile Leu Lys Asn Ala Thr Ile Gln Asp Gly Leu Val Ile End
    510             515             520
```

```
ATTTAATCAT AACCTCATTA GAAAGAAATA ATTTTGCATG ATTTCCTTTT        1823

CATGTAACCT AAACTGGCTA AACCACGAGG TTTTCTCATC TGTATATATA        1873

ATATGTCTAT AACTATGGAT AATCTTAATA AAAAAAAAAA AAAAAAAAAA        1923

A                                                            1924
```

The small subunit of the ADP-glucose-pyrophosphalase has
the following nucleotide sequence (Seq. ID No. 2):

```
GG ATA ACT GTG CCA TCA ACC TCC TCA AAG AAC CTC CAA AAT AGC    0044
   Ile Thr Val Pro Ser Thr Ser Ser Lys Asn Leu Gln Asn Ser
                5                   10
```

```
CTC GCA TTC TCC TCT TCT TCT CTC TCC GGC GAC AAA ATT CAA ACG   0089
Leu Ala Phe Ser Ser Ser Ser Leu Ser Gly Asp Lys Ile Gln Thr
15              20              25
```

```
ACG TCA TTT CTC AAC CGC CGA TAT TGT AGA ATC TCT TCT AGA GCT   0134
Thr Ser Phe Leu Asn Arg Arg Tyr Cys Arg Ile Ser Ser Arg Ala
30              35              40
```

11

```
CCG ATT GTT GTC TCT CCC AAA GCT GTT TCT GAT TCT AAG AAT TCG   0179
Pro Ile Val Val Ser Pro Lys Ala Val Ser Asp Ser Lys Asn Ser
 45              50              55


CAG ACT TGT CTT GAC CCT GAA GCC AGC CGT AGT GTT CTT GGT ATT   0224
Gln Thr Cys Leu Asp Pro Glu Ala Ser Arg Ser Val Leu Gly Ile
 60              65              70


ATA CTT GGA GGT GGT GCT GGT ACA CGT CTT TAC CCG TTG ACT AAG   0269
Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys
 75              80              85


AAG AGA GCC AAA CCA GCC GTG CCA CTC GGT GCT AAT TAT AGG CTT   0314
Lys Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu
 90              95              100


ATT GAT ATC CCA GTG AGC AAT TGT TTG AAC AGT AAT ATT TCC AAA   0359
Ile Asp Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys
105             110             110


ATA TAT GTT CTT ACA CAA TTC AAT TCT GCT TCT CTG AAT CGT CAT   0404
Ile Tyr Val Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His
115             120             125


CTT TCG CGG GCA TAT GCT AGC AAC ATG GGA GGA TAC AAA AAT GAG   0449
Leu Ser Arg Ala Tyr Ala Ser Asn Met Gly Gly Tyr Lys Asn Glu
130             135             140


GGG TTT GTA GAA GTT CTT GCT GCT CAG CAA AGT CCA GAG AAT CCA   0494
Gly Phe Val Glu Val Leu Ala Ala Gln Gln Ser Pro Glu Asn Pro
145             150             155
```

12

```
AAC TGG TTT CAG GGT ACA GCT GAT GCT GTT AGG CAA TAT CTG TGG     0539
Asn Trp Phe Gln Gly Thr Ala Asp Ala Val Arg Gln Tyr Leu Trp
160                 165                 170


CTT TTC GAA GAG CAC AAT GTT CTT GAG TAC TTG ATT CTT GCT GGT     0584
Leu Phe Glu Glu His Asn Val Leu Glu Tyr Leu Ile Leu Ala Gly
175                 180                 185


GAC CAT TTG TAT CGA ATG GAT TAT GAA AGA TTT GTC CAA GCT CAC     0629
Asp His Leu Tyr Arg Met Asp Tyr Glu Arg Phe Val Gln Ala His
190                 195                 200


AGA GAA ACT GAT GCA GAC ATT ACT GTT GCT GCA TTG CCA ATG GAT     0674
Arg Glu Thr Asp Ala Asp Ile Thr Val Ala Ala Leu Pro Met Asp
205                 210                 215


GAA AAG CGT GCT ACT GCA TTT GGT TTG ATG AAA ATT GAT GAA GAA     0719
Glu Lys Arg Ala Thr Ala Phe Gly Leu Met Lys Ile Asp Glu Glu
220                 225                 230


GGA AGA ATT ATT GAG TTT GCC GAG AAA CCG AAA GGA GAA CAA TTG     0764
Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro Lys Gly Glu Gln Leu
235                 240                 245


AAA GCT ATG AAG GTT GAT ACC ACA ATC CTG GGT CTG GAC GAT GAG     0809
Lys Ala Met Lys Val Asp Thr Thr Ile Leu Gly Leu Asp Asp Glu
250                 255                 260
```

13

```
AGA GCA AAA GAA ATG CCA TTC ATA GCC AGC ATG GGC ATA TAT GTT       0854
Arg Ala Lys Glu Met Pro Phe Ile Ala Ser Met Gly Ile Tyr Val
265             270             275


ATT AGC AAA GAT GTA ATG CTT AAT CTG CTT CGG GAG CAA TTT CCT       0899
Ile Ser Lys Asp Val Met Leu Asn Leu Leu Arg Glu Gln Phe Pro
280             285             290


GGT GCT AAT GAT TTT GGA AGT GAA GTT ATT CCA GGC GCC ACT TCC       0944
Gly Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr Ser
295             300             305


ATA GGG TTG AGA GTC CAA GCT TAT TTG TAT GAT GGT TAC TGG GAG       0989
Ile Gly Leu Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu
310             315             320


GAT ATT GGT ACC ATT GAA GCT TTT TAC AAT GCT AAC TTG GGA ATC       1034
Asp Ile Gly Thr Ile Glu Ala Phe Tyr Asn Ala Asn Leu Gly Ile
325             330             335


ACC AAA AAG CCG GTG CCA GAT TTT AGC TTC TAT GAT CGT TCA TCT       1079
Thr Lys Lys Pro Val Pro Asp Phe Ser Phe Tyr Asp Arg Ser Ser
340             345             350


CCA ATT TAT ACA CAA CCT CGG TAT TTG CCT CCT TCA AAG ATG CTT       1124
Pro Ile Tyr Thr Gln Pro Arg Tyr Leu Pro Pro Ser Lys Met Leu
355             360             365
```

14

```
GAT GCT GAT ATA ACT GAC AGC GTC ATC GGT GAA GGC TGT GTT ATT      1169
Asp Ala Asp Ile Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile
370                 375             380


AAG AAC TGT AAG ATT CAT CAT TCT GTT ATC GGA CTT CGA TCT TGT      1214
Lys Asn Cys Lys Ile His His Ser Val Ile Gly Leu Arg Ser Cys
385                 390             395


ATC TCG GAG GGT GCA ATC ATT GAG GAC ACA CTG TTG ATG GGA GCT      1259
Ile Ser Glu Gly Ala Ile Ile Glu Asp Thr Leu Leu Met Gly Ala
400                 405             410


GAT TAT TAT GAG ACT GAT GCT GAT CGG AAA TTC CTG GCT GCT AAG      1304
Asp Tyr Tyr Glu Thr Asp Ala Asp Arg Lys Phe Leu Ala Ala Lys
415                 420             425


GGT AGT GTA CCT ATT GGA ATT GGG AAT GCA CGT ATT GGG GAT GAT      1349
Gly Ser Val Pro Ile Gly Ile Gly Asn Ala Arg Ile Gly Asp Asp
430                 435             440


GTC AAG ATT ATC AAC AGT GAC AAT GTA CAA GAA GCA GCA AGA GAA      1394
Val Lys Ile Ile Asn Ser Asp Asn Val Gln Glu Ala Ala Arg Glu
445                 450             455


ACA GAC GGA TAC TTC ATA AAG AGC GGA ATA GTC ACT ATA ATC AAG      1439
Thr Asp Gly Tyr Phe Ile Lys Ser Gly Ile Val Thr Ile Ile Lys
460                 465             470
```

15

```
GAC GCC ATG ATT CCA AGT GGA ACT GTA ATC TAG AAATGGAGCA        1482
Asp Ala Met Ile Pro Ser Gly Thr Val Ile End
475             480             485
```

```
TATAATAAAT ATCACTGCCT ATTTACAGTA CCTATCTGAG TCTCCCACCA        1532

TGACCCTTTG ATTCAATCTT TTAGTTATGT AAATATTTTT GGCTTTTGCG        1582

ATTTTGCCAT AAATTTGAAG AAGCGAGGAT TCAGGGACGA TAGTGCTATG        1632

AATTGGAAGA AAGGATTTGG GGGATATCTT TGTAAAGACA TTTTGACTAC        1682

TGGGCACTAA AAATTTGGTA ATGCTATACC AAAATATATA AAAAGATCTT        1732
GCTGGGTTTT GGTAAAAAAA AAAAAAAAAA A                           1763
```

The sucrose phosphate - synthase has the following
nucleotide sequence (Seq. ID No. 3):

```
GGGCTGCAGG GAAGCTCTGA ACTTCAAAA ATG GCG GGA AAT GAT        0044
                                    Met Ala Gly Asn Asp
                                                      5
```

```
TGG ATA AAC AGT TAT TTA GAG GCA ATT CTG GAT GTG GGT CCA GGA     0089
Trp Ile Asn Ser Tyr Leu Glu Ala Ile Leu Asp Val Gly Pro Gly
                 10              15                  20
```

```
CTT GAT GAT GCA AAA TCA TCT TTG CTT TTG AGA GAA AGA GGC AGG     0134
Leu Asp Asp Ala Lys Ser Ser Leu Leu Leu Arg Glu Arg Gly Arg
                 25              30                  35
```

```
TTT AGT CCT ACT CGT TAC TTT GTT GAA GAA GTT ATC ACT GGT TTT     0179
Phe Ser Pro Thr Arg Tyr Phe Val Glu Glu Val Ile Thr Gly Phe
                 40              45                  50
```

16

```
GAT GAA ACC GAC CTT CAT CGT TCA TGG GTT CGG GCA CAA GCA ACA    0224
Asp Glu Thr Asp Leu His Arg Ser Trp Val Arg Ala Gln Ala Thr
            55                  60                  65


AGG AGT CCT CAA GAG AGG AAT ACT AGA TTG GAG AAC ATG TGT TGG    0269
Arg Ser Pro Gln Glu Arg Asn Thr Arg Leu Glu Asn Met Cys Trp
            70                  75                  80


AGA ATT TGG AAT TTG GCT CGT CAG AAG AAG CAG CTT GAG AAT GAA    0314
Arg Ile Trp Asn Leu Ala Arg Gln Lys Lys Gln Leu Glu Asn Glu
            85                  90                  95


GAA GCT CAG CGG AAG ACA AAA CGT CGT ATG GAG CTT GAG AGG GGT    0359
Glu Ala Gln Arg Lys Thr Lys Arg Arg Met Glu Leu Glu Arg Gly
            100                 105                 110


CGT CGA GAA GCA ACT GCT GAT ATG TCG GAG GAC TTA TCA GAA GGC    0404
Arg Arg Glu Ala Thr Ala Asp Met Ser Glu Asp Leu Ser Glu Gly
            115                 120                 125


GAA AAG GAC ATT TCA GCT CAT GGT GAT AGC ACC CGT CCT AGA TTG    0449
Glu Lys Asp Ile Ser Ala His Gly Asp Ser Thr Arg Pro Arg Leu
            130                 135                 140


CCA AGA ATA AAT TCT CTT GAT GCT ATG GAG ACA TGG ATT AGT CAA    0494
Pro Arg Ile Asn Ser Leu Asp Ala Met Glu Thr Trp Ile Ser Gln
            145                 150                 155


CAA AAG GAA AAA AAA CTC TAC CTT GTT TTG ATA AGT CTT CAT GGT    0539
Gln Lys Glu Lys Lys Leu Tyr Leu Val Leu Ile Ser Leu His Gly
            160                 165                 170
```

17

TTG ATA CGA GGT GAA AAC ATG GAA CTT GGC CGT GAT TCT GAT ACT   0584
Leu Ile Arg Gly Glu Asn Met Glu Leu Gly Arg Asp Ser Asp Thr
            175   180   185

GGT GGT CAG GTT AAG TAT GTG GTT GAG CTT GCA AGG GCT CTA GGT   0629
Gly Gly Gln Val Lys Tyr Val Val Glu Leu Ala Arg Ala Leu Gly
            190   195   200

TCG ATG CCA GGT GTT TAT AGA GTT GAT TTG CTA ACT AGG CAA GTT   0674
Ser Met Pro Gly Val Tyr Arg Val Asp Leu Leu Thr Arg Gln Val
            205   210   215

TCA TCT CCT GAC GTG GAT TGG AGT TAT GGG GAG CCT ACT GAG ATG   0719
Ser Ser Pro Asp Val Asp Trp Ser Tyr Gly Glu Pro Thr Glu Met
            220   225   230

CTG AAT CCA AGG GAT TCC AAT GGT TTT GAT GAT GAT GAT GAT GAA   0764
Leu Asn Pro Arg Asp Ser Asn Gly Phe Asp Asp Asp Asp Asp Glu
            235   240   245

ATG GGA GAG AGT AGT GGT GCT TAC ATT GTT CGT ATA CCA TTT GGG   0809
Met Gly Glu Ser Ser Gly Ala Tyr Ile Val Arg Ile Pro Phe Gly
            250   255   260

CCG AGG GAT AAG TAT ATC GCA AAA GAA GAG CTT TGG CCC TAT ATT   0854
Pro Arg Asp Lys Tyr Ile Ala Lys Glu Glu Leu Trp Pro Tyr Ile
            265   270   275

18

```
CCT GAA TTT GTT GAT GGT GCT CTA AAC CAC ATA GTT CAA ATG TCC   0899
Pro Glu Phe Val Asp Gly Ala Leu Asn His Ile Val Gln Met Ser
            280                 285                 290


AAA GTT TTA GGT GAG CAA ATT GGT AGC GGG GAA ACA GTT TGG CCA   0944
Lys Val Leu Gly Glu Gln Ile Gly Ser Gly Glu Thr Val Trp Pro
            295                 300                 305


GTT GCC ATT CAT GGA CAT TAT GCT GAT GCT GGT GAT TCT GCT GCT   0989
Val Ala Ile His Gly His Tyr Ala Asp Ala Gly Asp Ser Ala Ala
            310                 315                 320


CTT CTT TCT GGT GGC CTA AAT GTT CCA ATG CTT TTA ACG GGG CAT   1034
Leu Leu Ser Gly Gly Leu Asn Val Pro Met Leu Leu Thr Gly His
            325                 330                 335


TCT CTT GGC CGA GAC AAG TTA GAG CAG CTC CTC AAA CAG GGT CGA   1079
Ser Leu Gly Arg Asp Lys Leu Glu Gln Leu Leu Lys Gln Gly Arg
            340                 345                 350


ATG TCT AAA GAT GAC ATA AAC AAT ACA TAC AAA ATA ATG CGT AGG   1124
Met Ser Lys Asp Asp Ile Asn Asn Thr Tyr Lys Ile Met Arg Arg
            355                 360                 365


ATA GAA GCC GAA GAG TTA TCA CTT GAT GCC TCT GAG ATA GTC ATA   1169
Ile Glu Ala Glu Glu Leu Ser Leu Asp Ala Ser Glu Ile Val Ile
            370                 375                 380
```

19

```
ACT AGT ACA AGA CAA GAA ATA GAA GAG CAA TGG CAC CTC TAT GAT   1214
Thr Ser Thr Arg Gln Glu Ile Glu Glu Gln Trp His Leu Tyr Asp
            385                 390                 395


GGG TTT GAT CCT GTG CTA GAA CGT AAA CTC CGT GCT AGG ATG AAG   1259
Gly Phe Asp Pro Val Leu Glu Arg Lys Leu Arg Ala Arg Met Lys
            400                 405                 410


CGT GGT GTA AGC TGT TAT GGA AGG TTC ATG CCC CGG ATG GTT GTT   1304
Arg Gly Val Ser Cys Tyr Gly Arg Phe Met Pro Arg Met Val Val
            415                 420                 425


ATT CCT CCT GGA ATG GAA TTC AAT CAT ATT GTT CCA CAT GAG GGT   1349
Ile Pro Pro Gly Met Glu Phe Asn His Ile Val Pro His Glu Gly
            430                 435                 440


GAT ATG GAT GGT GAA ACA GAA GAA ACT GAA GAG CAT CCT ACA TCA   1394
Asp Met Asp Gly Glu Thr Glu Glu Thr Glu Glu His Pro Thr Ser
            445                 450                 455


CCT GAT CCA CCT ATC TGG GCT GAG ATT ATG CGC TTC TTT TCT AAA   1439
Pro Asp Pro Pro Ile Trp Ala Glu Ile Met Arg Phe Phe Ser Lys
            460                 465                 470


CCA AGG AAG CCA ATG ATA CTT GCC CTT GCT AGG CCT GAC CCG AAG   1484
Pro Arg Lys Pro Met Ile Leu Ala Leu Ala Arg Pro Asp Pro Lys
            475                 480                 485
```

20

```
AAG AAT ATC ACG ACT TTG GTC AAA GCA TTT GGA GAA TGC CGT CCA    1529
Lys Asn Ile Thr Thr Leu Val Lys Ala Phe Gly Glu Cys Arg Pro
            490             495                 500


CTA AGG GAG CTA GCT AAT CTT ACT CTT ATA ATG GGT AAC CGA GAT    1574
Leu Arg Glu Leu Ala Asn Leu Thr Leu Ile Met Gly Asn Arg Asp
            505             510                 515


GGT ATT GAC GAG ATG TCA AGC ACC AGT TCT TCA GTT CTC CTG TCA    1619
Gly Ile Asp Glu Met Ser Ser Thr Ser Ser Ser Val Leu Leu Ser
                520             525                 530


GTG CTT AAG CTA ATT GAT CAA TAC GAC CTT TAT GGT CAA GTA GCA    1664
Val Leu Lys Leu Ile Asp Gln Tyr Asp Leu Tyr Gly Gln Val Ala
            535             540                 545


TAC CCC AAA CAT CAC AAG CAA GCT GAT GTT CCT GAG ATT TAT CGT    1709
Tyr Pro Lys His His Lys Gln Ala Asp Val Pro Glu Ile Tyr Arg
            550             555                 600


TTG GCA GCA AAG ACA AAG GGA GTC TTT ATT AAT CCA GCT TTT ATT    1754
Leu Ala Ala Lys Thr Lys Gly Val Phe Ile Asn Pro Ala Phe Ile
            605             610                 615


GAG CCA TTT GGG CTG ACT CTA ATA GAG GCA GCA GCT CAT GGT TTA    1799
Glu Pro Phe Gly Leu Thr Leu Ile Glu Ala Ala Ala His Gly Leu
            620             625                 630
```

21

```
CCG ATG GTT GCT ACG AAA AAT GGA GGC CCT GTT GAT ATC CAG AGG   1844
Pro Met Val Ala Thr Lys Asn Gly Gly Pro Val Asp Ile Gln Arg
            635                 640                 645


GTC CTT GAT AAT GGT CTT CTT GTG GAT CCT CAT GAG CAG CAG TCT   1889
Val Leu Asp Asn Gly Leu Leu Val Asp Pro His Glu Gln Gln Ser
            650                 655                 660


ATT GCT ACT GCT TTG CTG AAG CTT GTT GCT GAT AAG CAA CTA TGG   1934
Ile Ala Thr Ala Leu Leu Lys Leu Val Ala Asp Lys Gln Leu Trp
            665                 670                 675


ACA AAA TGC CAG CAA AAT GGA CTG AAA AAT ATT CAT CTC TAC TCT   1979
Thr Lys Cys Gln Gln Asn Gly Leu Lys Asn Ile His Leu Tyr Ser
            680                 685                 690


TGG CCA GAG CAT TCG AAG ACA TAC CTA TCT CGA ATA GCC AGT TCG   2024
Trp Pro Glu His Ser Lys Thr Tyr Leu Ser Arg Ile Ala Ser Ser
            695                 700                 705


AGA CAA AGG CAA CCA CAG TGG CAA AGA AGT AGT GAT GAA GGG CTT   2069
Arg Gln Arg Gln Pro Gln Trp Gln Arg Ser Ser Asp Glu Gly Leu
            710                 715                 720


GAC AAT CAA GAG CCT GAA TCT CCA AGT GAT TCT TTA AGA GAT ATA   2114
Asp Asn Gln Glu Pro Glu Ser Pro Ser Asp Ser Leu Arg Asp Ile
            725                 730                 735
```

22

```
AAG GAT ATA TCT CTA AAC CTT GAA GTT CTC GTT AGA CCG GAG AAA   2159
Lys Asp Ile Ser Leu Asn Leu Glu Val Leu Val Arg Pro Glu Lys
            740               745               750


AGG GTG AAG ACG TTG AAA ATC TTG GGA TTG ATG ACA AAA GCA AAT   2204
Arg Val Lys Thr Leu Lys Ile Leu Gly Leu Met Thr Lys Ala Asn
            755               760               765


TCG AGA ATG CTG TTA TGT TCA TGG TCT AAT GGT GTC CAT AAG ATG   2249
Ser Arg Met Leu Leu Cys Ser Trp Ser Asn Gly Val His Lys Met
            770               775               780


CTT CGG AAG GCT CGG TTC TCT GAC AAA GTA GAT CAG GCT TCT AGT   2294
Leu Arg Lys Ala Arg Phe Ser Asp Lys Val Asp Gln Ala Ser Ser
            785               790               795


AAA TAT CCA GCA TTT AGG AGG AGA AAA CTT ATA TAT GTT ATT GCT   2339
Lys Tyr Pro Ala Phe Arg Arg Arg Lys Leu Ile Tyr Val Ile Ala
            800               805               810


GTA GAC GGG GAT TAT GAA GAT GGA CTT TTT GAT ATT GTT CGG AGG   2384
Val Asp Gly Asp Tyr Glu Asp Gly Leu Phe Asp Ile Val Arg Arg
            815               820               825


ATA TTT GAT GCT GCT GGC AAG GAG AAG ATT GAA GGT TCC ATC GGG   2429
Ile Phe Asp Ala Ala Gly Lys Glu Lys Ile Glu Gly Ser Ile Gly
            830               835               840
```

23

```
TTT ATA TTG TCA ACA TCC TAT TCT ATG CCC GAA ATT CAG AAC TAT   2474
Phe Ile Leu Ser Thr Ser Tyr Ser Met Pro Glu Ile Gln Asn Tyr
            845             850             855


TTG CTA TCA AAA GGC TTC AAT CTT CAT GAT TTT GAT GCA TAT ATA   2519
Leu Leu Ser Lys Gly Phe Asn Leu His Asp Phe Asp Ala Tyr Ile
            860             865             870


TGC AAC AGT GGG AGT GAG TTG TAC TAT TCA TCT TTG AAC TCA GAG   2564
Cys Asn Ser Gly Ser Glu Leu Tyr Tyr Ser Ser Leu Asn Ser Glu
            875             880             885


GAG AGT AAT ATT ATA GCA GAT TCA GAT TAC CAT TCA CAC ATA GAG   2609
Glu Ser Asn Ile Ile Ala Asp Ser Asp Tyr His Ser His Ile Glu
            890             895             900


TAC AGA TGG GGT GGA GAA GGC CTT AGA AGG ACT TTG CTT CGC TGG   2654
Tyr Arg Trp Gly Gly Glu Gly Leu Arg Arg Thr Leu Leu Arg Trp
            905             910             915


GCA GCT TCC ATC ACA GAA AAA AAT GGT GAA AAC GAA GAA CAG GTT   2699
Ala Ala Ser Ile Thr Glu Lys Asn Gly Glu Asn Glu Glu Gln Val
            920             925             930


ATT ACT GAA GAT GAA GAA GTT TCT ACG GGT TAT TGC TTT GCG TTT   2744
Ile Thr Glu Asp Glu Glu Val Ser Thr Gly Tyr Cys Phe Ala Phe
            935             940             945
```

24

```
AAA ATA AAG AAC CAA AAT AAG GTT CCC CCT ACG AAG GAG CTC CGC   2789
Lys Ile Lys Asn Gln Asn Lys Val Pro Pro Thr Lys Glu Leu Arg
            950                 955                 960


AAG TCA ATG AGG ATT CAA GCT CTT CGT TGC CAT GTG ATT TAC TGT   2834
Lys Ser Met Arg Ile Gln Ala Leu Arg Cys His Val Ile Tyr Cys
            965                 970                 975


CAG AAC GGA TCT AAA ATG AAT GTG ATT CCA GTA CTA GCA TCC CGT   2879
Gln Asn Gly Ser Lys Met Asn Val Ile Pro Val Leu Ala Ser Arg
            980                 985                 990


TCT CAA GCC CTC AGG TAT CTT TAT GTT CGT TGG GGA GTT GAG TTG   2924
Ser Gln Ala Leu Arg Tyr Leu Tyr Val Arg Trp Gly Val Glu Leu
            995                 1000                1005


TCG AAG ATG GTT GTC TTT GTT GGA GAA TGT GGT GAC ACA GAT TAT   2969
Ser Lys Met Val Val Phe Val Gly Glu Cys Gly Asp Thr Asp Tyr
            1010                1015                1020


GAA GGC TTG CTT GGC GGG GTC CAT AAA ACC GTA ATA CTG AAG GGA   3014
Glu Gly Leu Leu Gly Gly Val His Lys Thr Val Ile Leu Lys Gly
            1025                1030                1035


GTC TCC AAC ACT GCT TTA AGG TCT CTC CAT GCC AAC AGA AGT TAC   3059
Val Ser Asn Thr Ala Leu Arg Ser Leu His Ala Asn Arg Ser Tyr
            1040                1045                1050
```

25

```
CCT CTT TCA CAT GTC GTG TCG CTT GAC AGC CCC AAT ATT GGC GAG    3104
Pro Leu Ser His Val Val Ser Leu Asp Ser Pro Asn Ile Gly Glu
            1055                1060                1065


GTG AGC AAA GGG TGC AGC AGC TCC GAG ATC CAG TCC ATC GTC ACA    3149
Val Ser Lys Gly Cys Ser Ser Ser Glu Ile Gln Ser Ile Val Thr
            1070                1075                1080


AAA CTC TCC AAA GCT TAA TCAGATATCT GCTGCTTTCT TTTGGGTAAG       3197
Lys Leu Ser Lys Ala End
            1085
```

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CAAGGTTTCA TCTTATATGA TTATATCATA AGATACTATA TAAGCACCTT         3247

ATTGGTAAGT CAGTCCCATA ATAATAATGT ACTTCAGAAC CACAATACTT         3297

AAAAGTTGGT TCAGTAGTGA TTAGTCTCAT AATAATCATA TAATTACACA         3347

TCCGCTGTTA ACTAGTGGTA ATATCTAAGC TCAACAATAA AGATGTAAAA         3397

TGCTAGTATG GAAATGAATT GCTAGCTGTT GATCTCTTTC CCTTTATTCT         3447

GTATTATTTC TTTCCTCATC TCATGTAAAA ACAATTTTCT GAAGGTGTAC         3497

AGTTTTTTCC CCTTATATAT CTGTATTATT TCTACTATTT TTTGTTTGTA         3547

AGAATATCCT CTCATCGAGG AGTGATAATT AAATAACCGG CTTGCTAAAT         3597

ATAAAGCTTA TTCGAGTTAA AAAAAAAAAA AAAAAAAA                      3635
```

26

The sucrose-synthase has the following nucleotide sequence
(Seq. ID No. 4):

```
   CT GCA GGA GGG AAA CAA ATT CTT AGC GAT GGC CCG TTT AGC GAA     0044
      Ala Gly Gly Lys Gln Ile Leu Ser Asp Gly Pro Phe Ser Glu
                           5                   10


   GTT CTT AGG TCT GCT CAG GAA GCA ATA GTT GTT CCT CCC TTT GTT     0089
   Val Leu Arg Ser Ala Gln Glu Ala Ile Val Val Pro Pro Phe Val
   15                   20                  25


   GCT ATA GCA GTC CGT CCA AGA CCT GGA GTT TGG GAA TAT GTT CGT     0134
   Ala Ile Ala Val Arg Pro Arg Pro Gly Val Trp Glu Tyr Val Arg
   30                  35                  40


   GTT AAT GTC TCT GAA CTG AAT GTG GAG CAG CTA ACT GTG TCT GAG     0179
   Val Asn Val Ser Glu Leu Asn Val Glu Gln Leu Thr Val Ser Glu
   45                  50                  55


   TAT CTC CAT TTC AAG GAA GAA CTT GTG GAT GGA AAG GCT GAT GAC     0224
   Tyr Leu His Phe Lys Glu Glu Leu Val Asp Gly Lys Ala Asp Asp
   60                  65                  70


   CAC TAT GTG CTT GAG CTT GAT TTC GAG CCT TTT AAT GAA TCA GTT     0269
   His Tyr Val Leu Glu Leu Asp Phe Glu Pro Phe Asn Glu Ser Val
   75                  80                  85


   CCA CGT CCA ACT CGC TCT TCA TCA ATT GGT AAT GGT GTT CAG TTC     0314
   Pro Arg Pro Thr Arg Ser Ser Ser Ile Gly Asn Gly Val Gln Phe
   90                  95                  100


   CTC AAT CGG CAC CTG TCA TCA AGC ATG TTC TGC AAC AAA GAT TGC     0359
   Leu Asn Arg His Leu Ser Ser Ser Met Phe Cys Asn Lys Asp Cys
   105                 110                 115
```

27

```
TTG GAG CCG TTA CTT GAT TTT CTT AGA GTG CAC AAA CAT AAA GGA        0404
Leu Glu Pro Leu Leu Asp Phe Leu Arg Val His Lys His Lys Gly
120             125             130


GTT GTC ATG ATG TTG AAT GAT CGG ATA CAG ACT ATC CAG CGT CTT        0449
Val Val Met Met Leu Asn Asp Arg Ile Gln Thr Ile Gln Arg Leu
135             140             145


CAG TCT GCA TTG TCT AAA GCT GAG GAT TAT CTT ATC AAA CTT CCA        0494
Gln Ser Ala Leu Ser Lys Ala Glu Asp Tyr Leu Ile Lys Leu Pro
150             155             160


GCA GAT ACA CCT TAC TCT GAG TTC GAA TTT GTA ATC CAA GGT ATG        0539
Ala Asp Thr Pro Tyr Ser Glu Phe Glu Phe Val Ile Gln Gly Met
165             170             175


GGT TTT GAA AGA GGC TGG GGT GAT ACT GCT GAA AGG GTT CTA GAA        0584
Gly Phe Glu Arg Gly Trp Gly Asp Thr Ala Glu Arg Val Leu Glu
180             185             190


ATG ATG CAT CTA CTA CTA GAT ATC CTT CAG GCT CCC GAT CCG TCT        0629
Met Met His Leu Leu Leu Asp Ile Leu Gln Ala Pro Asp Pro Ser
195             200             205


ACA TTA GAG ACA TTT CTG GGA AGA CTT CCC ATG GTG TTT AAT GTG        0674
Thr Leu Glu Thr Phe Leu Gly Arg Leu Pro Met Val Phe Asn Val
210             215             220
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28

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GTC ATT TTG TCT GTA CAT GGA TAT TTT GGA CAG GCA CAT GTG CTC    0719
Val Ile Leu Ser Val His Gly Tyr Phe Gly Gln Ala His Val Leu
225                 230                 235


GGC TTG CCT GAC ACT GGT GGG CAG ATA GTT TAT ATA CTT GAC CAA    0764
Gly Leu Pro Asp Thr Gly Gly Gln Ile Val Tyr Ile Leu Asp Gln
240                 245                 250


GTG CGG TCT CTG GAA CAT GAA ATG CTC CAA CGA ATA AAG AAG CAA    0809
Val Arg Ser Leu Glu His Glu Met Leu Gln Arg Ile Lys Lys Gln
255                 260                 265


GGA CTA GAT GTG ACT CCT AGA ATT CTT ATC GTG AGT CGG TTG ATT    0854
Gly Leu Asp Val Thr Pro Arg Ile Leu Ile Val Ser Arg Leu Ile
270                 275                 280


CCT GAC GCT AAA GGG ACC ACG TGC AAT CAA CGT ATG GAG AAA GTC    0899
Pro Asp Ala Lys Gly Thr Thr Cys Asn Gln Arg Met Glu Lys Val
285                 290                 295


AGT GGA ACA GAG CAT GCT AGT ATC CTG AGA GTT CCT TTC CGA TCA    0944
Ser Gly Thr Glu His Ala Ser Ile Leu Arg Val Pro Phe Arg Ser
300                 305                 310


GAG AAA GGA ATC CTC CGC AAA TGG ATA TCT AGA TTT GAT GTA TGG    0989
Glu Lys Gly Ile Leu Arg Lys Trp Ile Ser Arg Phe Asp Val Trp
315                 320                 325
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29

```
CCT TAT TTA GAG ACC TTC ACT GAG GAT GCA GCT GGT GAA ATT ATT      1034
Pro Tyr Leu Glu Thr Phe Thr Glu Asp Ala Ala Gly Glu Ile Ile
330             335             340


GGC GAG TTG CAG GGT CGT CCA GAT CTG ATA ATT GGC AAC TAC AGC      1079
Gly Glu Leu Gln Gly Arg Pro Asp Leu Ile Ile Gly Asn Tyr Ser
345             350             355


GAT GGG AAT ATA GTT GCT TCT TTA TTG TCC CAC AAA ATG GGT GTC      1124
Asp Gly Asn Ile Val Ala Ser Leu Leu Ser His Lys Met Gly Val
360             365             370


ACC CAG TGC AAT ATA GCC CAT GCA TTG GAG AAA ACC AAG TAT CCA      1169
Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Thr Lys Tyr Pro
375             380             385


GAT TCT GAT ATT TAC TGG AAA AGA TTT GAG GAC AAA TAT CAC TTC      1214
Asp Ser Asp Ile Tyr Trp Lys Arg Phe Glu Asp Lys Tyr His Phe
390             395             400


TCG TGT CAA TTT TCA GCT GAC TTG ATG GCA ATG AAT CAT GCT GAT      1259
Ser Cys Gln Phe Ser Ala Asp Leu Met Ala Met Asn His Ala Asp
405             410             415


TTC ATC ATT ACG AGT ACT TAC CAA GAG ATA GCT GGA ACG AAG AAT      1304
Phe Ile Ile Thr Ser Thr Tyr Gln Glu Ile Ala Gly Thr Lys Asn
420             425             430
```

30

```
ACT GTT GGT CAA TAT GAA AGC CAT AAG GCC TTT ACT TTT CCG GGG      1349
Thr Val Gly Gln Tyr Glu Ser His Lys Ala Phe Thr Phe Pro Gly
435             440             445


CTG TAT CGG GTG GTT CAC GGG ATT GAT GTC TTT GAT CCC AAG TTT      1394
Leu Tyr Arg Val Val His Gly Ile Asp Val Phe Asp Pro Lys Phe
450             455             460


AAT ATT GTC TCG CCA GGG GCA GAC ATG GCC ATC TAC TTC CCA TTT      1439
Asn Ile Val Ser Pro Gly Ala Asp Met Ala Ile Tyr Phe Pro Phe
465             470             475


TCA GAG AAG GAT GTC ACC TGT CTC ACT TCA CTT CAT AGA CTT ATA      1484
Ser Glu Lys Asp Val Thr Cys Leu Thr Ser Leu His Arg Leu Ile
480             485             490


GAG CAG CTC CTA TTC AAA CCT GAG CAG AAC GAA GAA CAC ATT GGT      1529
Glu Gln Leu Leu Phe Lys Pro Glu Gln Asn Glu Glu His Ile Gly
495             500             505


GTA TTA GAT GAT ACC TCA AAG CCA ATT ATA TTT TCC ATG GCG AGG      1574
Val Leu Asp Asp Thr Ser Lys Pro Ile Ile Phe Ser Met Ala Arg
510             515             520


CTA GAC CGT GTG AAG AAT ATA ACA GGG CTG GTA GAG TGC TAT GGC      1619
Leu Asp Arg Val Lys Asn Ile Thr Gly Leu Val Glu Cys Tyr Gly
525             530             535
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31

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AAG AAT GCG AAA CTC AGG GAA CTG GCA AAC CTG GTT GTA GTG GCT    1664
Lys Asn Ala Lys Leu Arg Glu Leu Ala Asn Leu Val Val Val Ala
540             545             550


GGG TAC AAT GAT GTA AAA AAG TCG AAT GAC AGG GAG GAA ATT GCC    1709
Gly Tyr Asn Asp Val Lys Lys Ser Asn Asp Arg Glu Glu Ile Ala
555             560             565


GAA ATC GAG AAG ATG CAC AGG CTT ATA CAG GAG TAT AAT TTA AGA    1754
Glu Ile Glu Lys Met His Arg Leu Ile Gln Glu Tyr Asn Leu Arg
570             575             580


GGA CAA TTT CGC TGG ATT GCT TCT CAA ACA AAT AGA GTA CGA AAT    1799
Gly Gln Phe Arg Trp Ile Ala Ser Gln Thr Asn Arg Val Arg Asn
585             590             595


GGT GAA CTC TAT CGC TAC ATT TGT GAC AAA GGA GGT ATT TTT GCG    1844
Gly Glu Leu Tyr Arg Tyr Ile Cys Asp Lys Gly Gly Ile Phe Ala
600             605             610


CAG CCT GCA TTT TAT GAA GCA TTT GGG CTT ACA GTT GTT GAA GCC    1889
Gln Pro Ala Phe Tyr Glu Ala Phe Gly Leu Thr Val Val Glu Ala
615             620             625


ATG ACC TGT GGT CTT CCC ACA TTT GCT ACC TGC CAC GGT GGT CCA    1934
Met Thr Cys Gly Leu Pro Thr Phe Ala Thr Cys His Gly Gly Pro
630             635             640
```

32

```
GCT GAG ATT ATA GAA GAC GGT GTT TCA GGA TTT CAT ATC GAT CCA      1979
Ala Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro
645              650              655


TAT CAT GCT GAT CAG GCA GAA AAA ATG ACT GAA TTC TTT GTC AAG      2024
Tyr His Ala Asp Gln Ala Glu Lys Met Thr Glu Phe Phe Val Lys
660              665              670


TGC AGA GAG GAT CCA AAC TAC TGG ACT AAA ATC TCT GCA GGA GGG      2069
Cys Arg Glu Asp Pro Asn Tyr Trp Thr Lys Ile Ser Ala Gly Gly
675              680              685


TTA CTA AGG ATC AAA GAA AGA TAT ACC TGG CAA AAG TAT TCT GAA      2114
Leu Leu Arg Ile Lys Glu Arg Tyr Thr Trp Gln Lys Tyr Ser Glu
690              695              700


AGG TTA ATG ACA TTG GCA GGG GTG TAT GGT TTC TGG AAA TAT GTC      2159
Arg Leu Met Thr Leu Ala Gly Val Tyr Gly Phe Trp Lys Tyr Val
705              710              715


TCT AAA CTA GAG AGA AGA GAG ACA CGA CGT TAT CTT GAG ATG TTC      2204
Ser Lys Leu Glu Arg Arg Glu Thr Arg Arg Tyr Leu Glu Met Phe
720              725              730


TAC ATT TTG AAG TTC CGT GAT CTG GCC AAC TCT GTT CCG CTG GCA      2249
Tyr Ile Leu Lys Phe Arg Asp Leu Ala Asn Ser Val Pro Leu Ala
735              740              745
```

33

```
ACA GAT GAA GAG CCT TCT ACT ACT GAT GCA GTT GCG ACA TTC CGT     2294
Thr Asp Glu Glu Pro Ser Thr Thr Asp Ala Val Ala Thr Phe Arg
750                 755                 760


GGA CCT TGA ACGCTGCTGC TTACTGAGGT TCCAAGTTGT GTATATATTA          2343
Gly Pro End


CTGTGAAAGG AATAAGTGTA GCTACACAAA AGGTTCTCAA CTATTAGTAT           2393

CTTCTCTGTG TAAATAACGA GAGTGAAAAA TGTAATATTG TTGATGTCTT           2443

GAAAACTGAG TTTGCTTTGT TTATTTTTAA GTGTATGACA ATATGTATCA           2493

TATAACGGAT TCTTCAGTGA TCATATCAAA AACTACTGAC CATCGAAGTT           2543

AATGAAAATC GACAGCAACA                                            2563
```

5   These sequences can also be combined together in a
     suitable plasmid which leads to a combination of the
     individual characteristics, conditioned by the expression
     of the protein.

10   The promoter should ensure that the foreign gene is
     expressed in the plant. The promoter can be so chosen that
     the expression occurs only in specified tissues, at a
     determined time point in the plant's development or at a
     time point determined by outside influences. The promoter
15   can be homologous or heterologous to the plant. Suitable
     promoters are e.g. the promoter of the 35S RNA of the
     cauliflower mosaic virus, the patatin promoter B33
     (Rocha-Sosa et al. (1989) EMBO J 8: 23-29) or a promoter

34

that ensures an expression only in photosynthetically
active tissues. Other promoters can be used which ensure
an expression only in specified organs, such as the root,
tuber, seed, stem or specified cell types such as
5   mesophyllic, epidermal or transport cells.

The coding sequences described herein contain the
information for the formation of an mRNA for the large
subunit of the ADP-glucose-pyrophosphorylase and the
10   sucrose-phosphate-synthase (SPS) and a part of the
information for formation of the small subunit of the
ADP-glucose-pyrophosphorylase as well as the
sucrose-synthase, that are suitable for the formation of
anti-sense RNA to the corresponding genes. Whether a
15   translatable mRNA or an anti-sense nucleic acid is formed,
depends on the orientation of the coding sequence in
relation to the promoter. If the 3' end of the coding
sequence is fused to the 3' end of the promoter, an
anti-sense RNA results, and by fusion of the 5' end of the
20   coding to the 3' end of the promoter a translatable RNA
results. This latter leads to an increase of the enzyme
activity in the cell, whilst the first leads to a
reduction of the enzyme activity in the cell.

25   The coding sequence for the large and small subunit of the
ADP-glucose-pyrophosphorylase, the sucrose phosphate
synthase and the sucrose synthase can be one of those
described in this invention or can be one that is derived
by modifications of the sequences described above.
30   Thereby especially modifications of the sequences can be
considered which lead to by-passing of the plant's own
regulation mechanisms. Modifications to the DNA sequences
of the invention can be by known methods, such as e.g.
base exchange or targeted or non-targeted mutagenesis. The
35   so-formed derivatives of the DNA sequences of the
invention are also within the scope of the invention.

35

With plasmids, which contain one or more of the DNA
sequences of the invention, sugar beet can be transformed
with the object of raising and/or reducing the enzyme
activity and/or the change of the sucrose concentration.

5

For the introduction of the DNA sequences of the invention
in sugar beet, a large number of cloning vectors are
available, which contain a replication signal for *E. coli*
and a marker, which allows a selection of the transformed

10   cells.

According to the introduction method of the desired gene
in the plant, other DNA sequences may be suitable. Should
the Ti- or Ri-plasmid be used, e.g. for the transformation

15   of the plant cell, then at least the right boundary, often
however both the right and left boundary of the Ti- and
Ri-Plasmid T-DNA, is attached, as a flanking region, to
the gene being introduced. The use of T-DNA for the
transformation of plants cells has been intensively

20   researched and is well described in EP 120 516; Hoekama,
In: The Binary Plant Vector System, Offset-drukkerij
Kanters B.V. Alblasserdam, (1985), Chapter V; Fraley, et
al., Crit. Rev. Plant Sci., 4:1-46 and An et al. (1985)
EMBO J. 4: 277-287. Once the introduced DNA is integrated

25   in the genome, it is as a rule stable there and remains
also in the offspring of the original transformed cells.
It normally contains a selection marker, which induces
resistance in the transformed plant cells against a
biocide or antibiotic such as kanamycin, G 418, bleomycin,

30   hygromycin or phosphinotricin etc. The individual marker
employed should therefore allow the selection of
transformed cells from cells, which lack the introduced
DNA.

35   For the introduction of DNA into a plant, besides
transformation using *Agrobacteria,* there are many other

36

techniques available. These techniques include the fusion
·of protoplasts, microinjection of DNA and electroporation,
as well as ballistic methods and virus infection. From the
transformed plant material, whole plants can be
5   regenerated in a suitable medium, which contains
antibiotics or biocides for the selection. The resulting
plants can then be tested for the presence of introduced
DNA. No special demands are placed on the plasmids in
injection and electroporation. Simple plasmids, such as
10 e.g. pUC-derivatives can be used. Should however whole
plants be regenerated from such transformed cells the
presence of a selectable marker gene is necessary. The
transformed cells grow within the plants in the usual
manner (see also McCormick et al.(1986) Plant Cell Reports
15 5: 81-84). These plants can be grown normally and crossed
with plants, that possess the same transformed genes or
different. The resulting hybrid individuals have the
corresponding phenotypical properties.

20

In order to understand the examples forming the basis of
this invention all the processes necessary for these tests
and which are known per se will first of all be listed:

25 1.   Cloning process
The vectors pUC 18/19 and M13mp10 series (Yanisch-Perron
et al. (1985) Gene 33: 103-119), as well as the vector
EMBL 3 (Frischauf et al. (1983) J Mol Biol 170: 827- 842)
were used for cloning.
30
For the plant transformations, the gene constructs were
cloned in the binary vector BIN 19 (Bevan (1984) Nucl.
Acids Res 12: 8711-8720)

35

2.   Bacterial strains

37

The *E. coli* strain BMH71-18 (Messing et al., Proc. Natl.
Acad. Sci. USA (1977), 24, 6342-6346) or TB1 was used for
the pUC and M13 mP vectors.

5   For the vector BIN19, the *E. coli* strain TB1 exclusively,
was used. TB1 is a recombinant-negative, tetracycline-
resistant derivative of strain JM101 (Yanisch-Perron et
al., Gene (1985), 33, 103-119). The genotype of the TB1
strain is (Bart Barrel, personal communication):
10   F'(traD36, proAB, lacI, lacZΔM15), Δ(lac, pro), SupE,
thiS, recA, Sr1::Tn10(TcR).

The transformation of the plasmids into the potato plants
was carried out using *Agrobacterium tumefaciens* strain
15   LBA4404 (Bevan, (1984), Nucl. Acids Res. 12, 8711-8720).

3. Transformation of *Agrobacterium tumefaciens*

In the case of BIN19 derivatives, the insertion of the DNA
20   into the *Agrobacterium* was effected by direct
transformation in accordance with the method of Holsters
et al., (1978) (Mol Gene Genet 163: 181-187). The plasmid
DNA of the transformed *Agrobacterium* was isolated in
accordance with the method of Birnboim and Doly (1979)
25   (Nucl Acids Res 7: 1513-1523) and was analysed by gel
electrophoresis after suitable restriction cleavage.

4. Sucrose phosphate-synthase activity test

30   The sucrose phosphate-synthase activity was determined
according to the method of Siegel and Stitt (1990, Plant
Science 66: 205-210) in a two stage analysis. To 180 μl of
a solution of 50mM HEPES/KOH (pH 7.4), 5mM magnesium
chloride, 5mM fructose-6-phosphate, 25mM
35   glucose-6-phosphate and 6mM uridine-5'-diphosphoglucose,
20 μl of probe was added and incubated for 10 minutes at

38

25°C. It was heated for 3 minutes at 95°C, to complete the
reaction. After centrifuging, the supernatant was
spectroscopically analysed for the liberation of
uridine-5'-diphosphate, whereby a pyruvate-kinase coupling

5   enzyme reaction was used. Preparations without hexose
phosphate, as well as the measurement of the recovery of
added uridine-5'-diphosphate act as controls.

Examples

10

Example 1

Cloning of cDNA to large and small subunits of the ADP
glucose pyrophosphorylase of sugar beet.

15

From the storage roots of 3-4 month old sugar beet plants
grown in the greenhouse, RNA was isolated according to the
method of Logemann et al (1987, Anal Biochem 163, 16-20).
Resulting from poly-A+-RNA, a cDNA library was laid down

20   according to the method of Gubler and Hoffmann (1983, Gene
25, 263) in the expression vector Lambda Zap II XR. To
this there was used an oligo-dT primer provided with an
XhoI recognising position and for synthesis of the first
cDNA strand methylated cytidine nucleotide was inserted.

25   After synthesis of the two strands an EcoRI-adaptor was
attached and removed to one side by again cutting with the
restriction endonuclease XhoI. In this way the
hemimethylation of cDNA was hindered so that an internal
XhoI recognition position is cut. By these procedures

30   there is obtained a population of cDNA molecules, that can
be cloned directed into the EcoRI/XhoI cut DNA of the
phage Lambda. After packing of recombinant phage-DNA in
phage heads, 200000 plaque forming units of the bank were
plated out for infection of a bacterial colony and then

35   each is probed with the total cDNA fragment of the large
and/or subunit of the AGPase of potato (Müller-Roeber et

39

al., 1990, MGG 224, 136-146) as an EcoRI-fragment. The
recombinant phages corresponding to the hybridising signal
were isolated. By *in vivo* excision plasmids were cut out
from the Lambda zap-genome, which carry a double stranded
5   cDNA as insertion. The plasmids were transformed in
bacterial cells. The plasmid-DNA was then propagated in
the bacteria. After checking the size of the insertions
individual clones were analysed by determination of the
primary sequence.
10

Example 2

Cloning of cDNA to sucrose-phosphate-synthase (SPS) from
15   sugar beet.

From the storage roots of 3-4 month old sugar beet plants
grown in the greenhouse, RNA was isolated according to the
method of Logemann et al (1987, Anal Biochem 163, 16-20).
20   Resulting from poly-A+-RNA, a cDNA library was laid down
according to the method of Gubler and Hoffmann (1983, Gene
25, 263) in the expression vector Lambda Zap II XR. To
this there was used an oligo-dT primer provided with an
XhoI recognising position and for synthesis of the first
25   cDNA strand methylated cytidine nucleotide was inserted.
After synthesis of the two strands an EcoRI-adaptor was
attached and removed to one side by again cutting with the
restriction endonuclease XhoI. In this way the
hemimethylation of cDNA was hindered so that an internal
30   XhoI recognition position is cut. By these procedures
there is obtained a population of cDNA molecules, that can
be cloned directed into the EcoRI/XhoI cut DNA of the
phage Lambda. After packing of recombinant phage-DNA in
phage heads, 200000 plaque forming units of the bank were
35   plated out for infection of a bacterial colony and then
each is probed with the total cDNA fragment of the

40

sucrose-phosphate-synthase (SPS) from spinach (Sonnewald,
1992, Planta) as NotI. The recombinant phages
corresponding to the hybridising signal were isolated. By
in vivo excision plasmids were cut out from the Lambda
5   zap-genome, which carry a double stranded cDNA as
insertion. The plasmids were transformed in bacterial
cells. The plasmid-DNA was then propagated in the
bacteria. After checking the size of the insertions
individual clones were analysed by determination of the
10   primary sequence.

Example 3

Cloning of cDNA to sucrose-synthase from sugar beet.
15

From the storage roots of 3-4 month old sugar beet plants
grown in the greenhouse, RNA was isolated according to the
method of Logemann et al (1987, Anal Biochem 163, 16-20).
Resulting from poly-A+-RNA, a cDNA library was laid down
20   according to the method of Gubler and Hoffmann (1983, Gene
25, 263) in the expression vector Lambda Zap II XR. To
this there was used an oligo-dT primer provided with an
XhoI recognising position and for synthesis of the first
cDNA strand methylated cytidine nucleotide was inserted.
25   After synthesis of the two strands an EcoRI-adaptor was
attached and removed to one side by again cutting with the
restriction endonuclease XhoI. In this way the
hemimethylation of cDNA was hindered so that an internal
XhoI recognition position is cut. By these procedures
30   there is obtained a population of cDNA molecules, that can
be cloned directed into the EcoRI/XhoI cut DNA of the
phage Lambda. After packing of recombinant phage-DNA in
phage heads, 200000 plaque forming units of the bank were
plated out for infection of a bacterial colony and then
35   parallel is probed with both EcoRI/BglIII sub fragments
sucrose synthase from maize (Worrell et al., 1991, Plant

41

Cell 3, 1121-1130). The recombinant phages corresponding
to the hybridising signal were isolated. By *in vivo*
excision plasmids were cut out from the Lambda zap-genome,
which carry a double stranded cDNA as insertion. The
5   plasmids were transformed in bacterial cells. The
plasmid-DNA was then propagated in the bacteria. After
checking the size of the insertions individual clones were
analysed by determination of the primary sequence.

10   Example 4

Determination of the nucleotide sequence of the ADP
glucose pyrophosphorylase, the sucrose synthase and the
sucrose phosphate synthase of sugar beet and derivation of
15   the corresponding amino acid sequences

The nucleotide sequences of the insertions obtained from
Examples 1 -3, were determined by standard methods by
means of the dideoxy method (Sanger et al. (1977) Proc.
20   Natl. Acad. Sci. USA, 74, 5463-5467). The nucleotide
sequences and the amino acid sequences derived therefrom
are given in the sequence protocols Seq. ID No. 1-4.

The sequences are shown earlier; the protocols are as
25   follows:

42

<u>SEQ ID NO: 1</u>
SEQUENCE TYPE: Nucleotide with corresponding protein
SEQUENCE LENGTH: 1924 base pairs

5   STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

ORIGINAL SOURCE
10 ORGANISM: *Beta vulgaris*
IMMEDIATE EXPERIMENTAL SOURCE: cDNA library in Phage Lamda
zap

FEATURES:
15 from 206 to 1770 coding region

PROPERTIES: ADP-glucose-pyrophosphorylase, large subunit

20 <u>SEQ ID NO: 2</u>
SEQUENCE TYPE: Nucleotide with corresponding protein
SEQUENCE LENGTH: 1763 base pairs

STRANDEDNESS: single
25 TOPOLOGY: linear
MOLECULE TYPE: cDNA

ORIGINAL SOURCE
ORGANISM: *Beta vulgaris*
30 IMMEDIATE EXPERIMENTAL SOURCE: cDNA library in Phage Lamda
zap

FEATURES:
from 3 to 1469 coding region

35

PROPERTIES: ADP-glucose-pyrophosphorylase, small subunit

43

SEQ ID NO: 3
SEQUENCE TYPE: Nucleotide with corresponding protein
SEQUENCE LENGTH: 3635 base pairs

5   STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

ORIGINAL SOURCE
10   ORGANISM: Beta vulgaris
IMMEDIATE EXPERIMENTAL SOURCE: cDNA library in Phage Lamda
zap

FEATURES:
15   from 31 to 3164 coding region

PROPERTIES: Sucrose-phosphate-synthase

20   SEQ ID NO: 4
SEQUENCE TYPE: Nucleotide with corresponding protein
SEQUENCE LENGTH: 2563 base pairs

STRANDEDNESS: single
25   TOPOLOGY: linear
MOLECULE TYPE: cDNA

ORIGINAL SOURCE
ORGANISM: Beta vulgaris
30   IMMEDIATE EXPERIMENTAL SOURCE: cDNA library in Phage Lamda
zap

FEATURES:
from 3 to 2300 coding region

35

PROPERTIES: Sucrose synthase

44

CLAIMS

1.   DNA sequence with the coding region for die large
      subunit of ADP-glucose-pyrophosphorylase for the
5   preparation of sugar beet with changed sucrose
      concentration, characterised in that the sequence
      has the following nucleotide sequence (Seq. ID
      No.1):

CAAAAGAAAA ACTTCCCATT TCTACTTCTT TGCACAATAT AATTTCCCAC   0050

CAATTTTTCT TTAAATTTCT CACTTTCATT TAATCAGTTT TCAGCAACAT   0100

TCTGATACTC GACAACCCAC TTTCTGTTCT CCCAAGATTC CAAACCTCTG   0150

ATTCTCATTC CACTAATATT TTTGCTTATT TTTTTTCTGG ATTTAAAGAA   0200

AAGCT ATG GAT GCA AGT GCA GCA GCC ATA AAT GTC AAT GCC CAT   0243
      Met Asp Ala Ser Ala Ala Ala Ile Asn Val Asn Ala His
                         5   10

TTA ACA GAA GTT GGA AAG AAA CGT TTT TTA GGA GAG AGA ATC AGT 0288
Leu Thr Glu Val Gly Lys Lys Arg Phe Leu Gly Glu Arg Ile Ser
    15   20   25

CAA AGT TTG AAG GGT AAA GAT CTG AGA GCT CTG TTT TCA AGA ACT 0333
Gln Ser Leu Lys Gly Lys Asp Leu Arg Ala Leu Phe Ser Arg Thr
    30   35   40

GAG AGC AAG GGT AGA AAT GTC AAT AAA CCT GGG GTT GCA TTT TCT 0378
Glu Ser Lys Gly Arg Asn Val Asn Lys Pro Gly Val Ala Phe Ser
    45   50   55

GTT CTC ACC TCA GAT TTT AAT CAA AGT GTT AAA GAA TCT TTG AAA 0423
Val Leu Thr Ser Asp Phe Asn Gln Ser Val Lys Glu Ser Leu Lys
    60   65   70

45

```
TAT GAG CCA GCA TTA TTT GAA TCT CCA AAA GCT GAC CCA AAA AAT   0468
Tyr Glu Pro Ala Leu Phe Glu Ser Pro Lys Ala Asp Pro Lys Asn
    75              80              85


GTG GCT GCA ATT GTG CTG GGT GGT GGT GCT GGG ACT CGC CTC TTT   0513
Val Ala Ala Ile Val Leu Gly Gly Gly Ala Gly Thr Arg Leu Phe
    90              95              100


CCT CTT ACT AGC AGG AGA GCT AAG CCA GCA GTG CCA ATT GGA GGG   0558
Pro Leu Thr Ser Arg Arg Ala Lys Pro Ala Val Pro Ile Gly Gly
    105             110             115



TGT TAC AGG CTG ATT GAT GTG CCT ATG AGC AAC TGC ATC AAC AGT   0603
Cys Tyr Arg Leu Ile Asp Val Pro Met Ser Asn Cys Ile Asn Ser
    120             125             130



GGC ATT AGA AAG ATT TTC ATT CTT ACC CAG TTC AAT TCG TTT TCG   0648
Gly Ile Arg Lys Ile Phe Ile Leu Thr Gln Phe Asn Ser Phe Ser
    135             140             145



CTT AAT CGT CAT CTT GCT CGA ACC TAT AAT TTT GGA GAT GGT GTG   0693
Leu Asn Arg His Leu Ala Arg Thr Tyr Asn Phe Gly Asp Gly Val
    150             155             160



AAT TTT GGG GAT GGC TTT GTG GAG GTT TTT GCT GCT ACA CAA ACA   0738
Asn Phe Gly Asp Gly Phe Val Glu Val Phe Ala Ala Thr Gln Thr
    165             170             175
```

46

```
CCT GGA GAA TCA GGA AAG AAA TGG TTC CAG GGC ACC GCT GAT GCA   0783
Pro Gly Glu Ser Gly Lys Lys Trp Phe Gln Gly Thr Ala Asp Ala
    180             185             190
```

```
GTA AGA CAG TTT TTC TGG GCA TTT GAG GAT TCC AAA TCC AAG GAT   0828
Val Arg Gln Phe Phe Trp Ala Phe Glu Asp Ser Lys Ser Lys Asp
    195             200             205
```

```
GTC GAG CAT ATA GTT ATT TTA TCC GGT GAT CAT CTT TAC CGA ATG   0873
Val Glu His Ile Val Ile Leu Ser Gly Asp His Leu Tyr Arg Met
    210             215             220
```

```
GAT TAC ATG AGT TTT TGG CAG AAG CAC ATT GAC ACC AAT GCT GAT   0918
Asp Tyr Met Ser Phe Trp Gln Lys His Ile Asp Thr Asn Ala Asp
    225             230             235
```

```
ATT ACA GTG TCA TGC ATA CCC ATG GAT GAC AGC CGT GCA TCG GAT   0963
Ile Thr Val Ser Cys Ile Pro Met Asp Asp Ser Arg Ala Ser Asp
    240             245             250
```

```
TAT GGG CTG ATG AAG ATT GAT CAC ACT GGA CGC ATT GTC CAT TTT   1008
Tyr Gly Leu Met Lys Ile Asp His Thr Gly Arg Ile Val His Phe
    255             260             265
```

```
GCA GAA AAA CCC AAG GGT TCT GAT CTA ACA GCA ATG CAA GTA GAT   1053
Ala Glu Lys Pro Lys Gly Ser Asp Leu Thr Ala Met Gln Val Asp
    270             275             280
```

47

```
ACA ACT GTT CTT GGG CTC TCT GAC CTT GAA GCT ATG TCA AAT CCA   1098
Thr Thr Val Leu Gly Leu Ser Asp Leu Glu Ala Met Ser Asn Pro
    285                 290                 295


TAT ATT GCA TCA ATG GGT GTT TAT GTC TTT CGA ACG GAT GTT CTT   1143
Tyr Ile Ala Ser Met Gly Val Tyr Val Phe Arg Thr Asp Val Leu
    300                 305                 310


ATG GAG CTT CTC AAT CGA AAA TAC CCT TCA AGC AAT GAT TTT GGC   1188
Met Glu Leu Leu Asn Arg Lys Tyr Pro Ser Ser Asn Asp Phe Gly
    315                 320                 325


TCT GAG ATT ATT CCT TCA GCT GTA GGA GAG TCT AAT GTT CAG GCA   1233
Ser Glu Ile Ile Pro Ser Ala Val Gly Glu Ser Asn Val Gln Ala
    330                 335                 340


TAT CTA TTT AAT GAC TAC TGG GAG GAT ATC GGA ACC ATA AAG TCT   1278
Tyr Leu Phe Asn Asp Tyr Trp Glu Asp Ile Gly Thr Ile Lys Ser
    345                 350                 355


TTC TTT GAT TCC AAT TTG GCC CTT ACA CAA CAG CCT CCC AAG TTT   1323
Phe Phe Asp Ser Asn Leu Ala Leu Thr Gln Gln Pro Pro Lys Phe
    360                 365                 370


GAA TTC TAC GAT CCA AAA ACA CCT TTT TAT ACA TCT GCA AGA TTT   1368
Glu Phe Tyr Asp Pro Lys Thr Pro Phe Tyr Thr Ser Ala Arg Phe
    375                 380                 385
```

48

```
CTG CCT CCT ACA AAA GTC GAC AGG TGC AAG ATT GTC GAT TCC ATT    1413
Leu Pro Pro Thr Lys Val Asp Arg Cys Lys Ile Val Asp Ser Ile
    390             395             400


GTA TCC CAT GGT TGT TTT CTA CAG GAG TCT AGC ATC CAA CAT TCC    1458
Val Ser His Gly Cys Phe Leu Gln Glu Ser Ser Ile Gln His Ser
    405             410             415


ATT GTT GGT GTT CGC TCA AGA TTA GAG TCC GGG GTT GAG TTC CAG    1503
Ile Val Gly Val Arg Ser Arg Leu Glu Ser Gly Val Glu Phe Gln
    420             425             430


GAC ACC ATG ATG ATG GGC GCA GAT TAC TAT CAA ACT GAA TCA GAA    1548
Asp Thr Met Met Met Gly Ala Asp Tyr Tyr Gln Thr Glu Ser Glu
    435             440             445


ATT GCT TCT CTG CTT GCT GAG GGA AAG GTT CCT GTT GGT GTC GGA    1593
Ile Ala Ser Leu Leu Ala Glu Gly Lys Val Pro Val Gly Val Gly
    450             455             460


CAG AAT ACC AAA ATA AAG AAT TGC ATA ATT GAC AAG AAC GCC AAA    1638
Gln Asn Thr Lys Ile Lys Asn Cys Ile Ile Asp Lys Asn Ala Lys
    465             470             475


ATT GGA AAA GAT GTG GTA ATC GCA AAC ACG GAT GGT GTT GAG GAA    1683
Ile Gly Lys Asp Val Val Ile Ala Asn Thr Asp Gly Val Glu Glu
    480             485             490
```

49

```
GCA GAT AGA CCA AAT GAA GGC TTT TAC ATC AGG TCG GGC ATT ACC   1728
Ala Asp Arg Pro Asn Glu Gly Phe Tyr Ile Arg Ser Gly Ile Thr
    495             500             505
```

```
ATC ATT TTG AAG AAC GCA ACC ATA CAA GAC GGT CTT GTG ATT TAG   1773
Ile Ile Leu Lys Asn Ala Thr Ile Gln Asp Gly Leu Val Ile End
    510             515             520
```

```
ATTTAATCAT AACCTCATTA GAAAGAAATA ATTTTGCATG ATTTCCTTTT         1823

CATGTAACCT AAACTGGCTA AACCACGAGG TTTTCTCATC TGTATATATA         1873

ATATGTCTAT AACTATGGAT AATCTTAATA AAAAAAAAAA AAAAAAAAAA         1923

A                                                             1924
```

2.   DNA sequence with the coding region for the small subunit of the
     ADP-glucose-pyrophosphalase for the preparation of sugar beet
     with changed sucrose concentration, characterised in that the
     sequence has the following nucleotide sequence (Seq. ID No.2):

```
GG ATA ACT GTG CCA TCA ACC TCC TCA AAG AAC CTC CAA AAT AGC     0044
   Ile Thr Val Pro Ser Thr Ser Ser Lys Asn Leu Gln Asn Ser
                   5               10
```

```
CTC GCA TTC TCC TCT TCT TCT CTC TCC GGC GAC AAA ATT CAA ACG    0089
Leu Ala Phe Ser Ser Ser Ser Leu Ser Gly Asp Lys Ile Gln Thr
15              20              25
```

```
ACG TCA TTT CTC AAC CGC CGA TAT TGT AGA ATC TCT TCT AGA GCT    0134
Thr Ser Phe Leu Asn Arg Arg Tyr Cys Arg Ile Ser Ser Arg Ala
30              35              40
```

50

```
CCG ATT GTT GTC TCT CCC AAA GCT GTT TCT GAT TCT AAG AAT TCG   0179
Pro Ile Val Val Ser Pro Lys Ala Val Ser Asp Ser Lys Asn Ser
45              50                  55


CAG ACT TGT CTT GAC CCT GAA GCC AGC CGT AGT GTT CTT GGT ATT   0224
Gln Thr Cys Leu Asp Pro Glu Ala Ser Arg Ser Val Leu Gly Ile
60              65                  70


ATA CTT GGA GGT GGT GCT GGT ACA CGT CTT TAC CCG TTG ACT AAG   0269
Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys
75              80                  85


AAG AGA GCC AAA CCA GCC GTG CCA CTC GGT GCT AAT TAT AGG CTT   0314
Lys Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu
90              95                  100


ATT GAT ATC CCA GTG AGC AAT TGT TTG AAC AGT AAT ATT TCC AAA   0359
Ile Asp Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys
105             110                 110


ATA TAT GTT CTT ACA CAA TTC AAT TCT GCT TCT CTG AAT CGT CAT   0404
Ile Tyr Val Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His
115             120                 125


CTT TCG CGG GCA TAT GCT AGC AAC ATG GGA GGA TAC AAA AAT GAG   0449
Leu Ser Arg Ala Tyr Ala Ser Asn Met Gly Gly Tyr Lys Asn Glu
130             135                 140


GGG TTT GTA GAA GTT CTT GCT GCT CAG CAA AGT CCA GAG AAT CCA   0494
Gly Phe Val Glu Val Leu Ala Ala Gln Gln Ser Pro Glu Asn Pro
145             150                 155
```

51

```
AAC TGG TTT CAG GGT ACA GCT GAT GCT GTT AGG CAA TAT CTG TGG   0539
Asn Trp Phe Gln Gly Thr Ala Asp Ala Val Arg Gln Tyr Leu Trp
160                 165                 170


CTT TTC GAA GAG CAC AAT GTT CTT GAG TAC TTG ATT CTT GCT GGT   0584
Leu Phe Glu Glu His Asn Val Leu Glu Tyr Leu Ile Leu Ala Gly
175                 180                 185


GAC CAT TTG TAT CGA ATG GAT TAT GAA AGA TTT GTC CAA GCT CAC   0629
Asp His Leu Tyr Arg Met Asp Tyr Glu Arg Phe Val Gln Ala His
190                 195                 200


AGA GAA ACT GAT GCA GAC ATT ACT GTT GCT GCA TTG CCA ATG GAT   0674
Arg Glu Thr Asp Ala Asp Ile Thr Val Ala Ala Leu Pro Met Asp
205                 210                 215


GAA AAG CGT GCT ACT GCA TTT GGT TTG ATG AAA ATT GAT GAA GAA   0719
Glu Lys Arg Ala Thr Ala Phe Gly Leu Met Lys Ile Asp Glu Glu
220                 225                 230


GGA AGA ATT ATT GAG TTT GCC GAG AAA CCG AAA GGA GAA CAA TTG   0764
Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro Lys Gly Glu Gln Leu
235                 240                 245


AAA GCT ATG AAG GTT GAT ACC ACA ATC CTG GGT CTG GAC GAT GAG   0809
Lys Ala Met Lys Val Asp Thr Thr Ile Leu Gly Leu Asp Asp Glu
250                 255                 260
```

52

```
AGA GCA AAA GAA ATG CCA TTC ATA GCC AGC ATG GGC ATA TAT GTT      0854
Arg Ala Lys Glu Met Pro Phe Ile Ala Ser Met Gly Ile Tyr Val
265             270             275


ATT AGC AAA GAT GTA ATG CTT AAT CTG CTT CGG GAG CAA TTT CCT      0899
Ile Ser Lys Asp Val Met Leu Asn Leu Leu Arg Glu Gln Phe Pro
280             285             290


GGT GCT AAT GAT TTT GGA AGT GAA GTT ATT CCA GGC GCC ACT TCC      0944
Gly Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr Ser
295             300             305


ATA GGG TTG AGA GTC CAA GCT TAT TTG TAT GAT GGT TAC TGG GAG      0989
Ile Gly Leu Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu
310             315             320


GAT ATT GGT ACC ATT GAA GCT TTT TAC AAT GCT AAC TTG GGA ATC      1034
Asp Ile Gly Thr Ile Glu Ala Phe Tyr Asn Ala Asn Leu Gly Ile
325             330             335


ACC AAA AAG CCG GTG CCA GAT TTT AGC TTC TAT GAT CGT TCA TCT      1079
Thr Lys Lys Pro Val Pro Asp Phe Ser Phe Tyr Asp Arg Ser Ser
340             345             350


CCA ATT TAT ACA CAA CCT CGG TAT TTG CCT CCT TCA AAG ATG CTT      1124
Pro Ile Tyr Thr Gln Pro Arg Tyr Leu Pro Pro Ser Lys Met Leu
355             360             365
```

53

```
GAT GCT GAT ATA ACT GAC AGC GTC ATC GGT GAA GGC TGT GTT ATT    1169
Asp Ala Asp Ile Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile
370             375             380


AAG AAC TGT AAG ATT CAT CAT TCT GTT ATC GGA CTT CGA TCT TGT    1214
Lys Asn Cys Lys Ile His His Ser Val Ile Gly Leu Arg Ser Cys
385             390             395


ATC TCG GAG GGT GCA ATC ATT GAG GAC ACA CTG TTG ATG GGA GCT    1259
Ile Ser Glu Gly Ala Ile Ile Glu Asp Thr Leu Leu Met Gly Ala
400             405             410


GAT TAT TAT GAG ACT GAT GCT GAT CGG AAA TTC CTG GCT GCT AAG    1304
Asp Tyr Tyr Glu Thr Asp Ala Asp Arg Lys Phe Leu Ala Ala Lys
415             420             425


GGT AGT GTA CCT ATT GGA ATT GGG AAT GCA CGT ATT GGG GAT GAT    1349
Gly Ser Val Pro Ile Gly Ile Gly Asn Ala Arg Ile Gly Asp Asp
430             435             440


GTC AAG ATT ATC AAC AGT GAC AAT GTA CAA GAA GCA GCA AGA GAA    1394
Val Lys Ile Ile Asn Ser Asp Asn Val Gln Glu Ala Ala Arg Glu
445             450             455


ACA GAC GGA TAC TTC ATA AAG AGC GGA ATA GTC ACT ATA ATC AAG    1439
Thr Asp Gly Tyr Phe Ile Lys Ser Gly Ile Val Thr Ile Ile Lys
460             465             470
```

54

```
GAC GCC ATG ATT CCA AGT GGA ACT GTA ATC TAG AAATGGAGCA        1482
Asp Ala Met Ile Pro Ser Gly Thr Val Ile End
475             480             485
```


```
TATAATAAAT ATCACTGCCT ATTTACAGTA CCTATCTGAG TCTCCCACCA        1532
```


```
TGACCCTTTG ATTCAATCTT TTAGTTATGT AAATATTTTT GGCTTTTGCG        1582
```


```
ATTTTGCCAT AAATTTGAAG AAGCGAGGAT TCAGGGACGA TAGTGCTATG        1632
```


```
AATTGGAAGA AAGGATTTGG GGGATATCTT TGTAAAGACA TTTTGACTAC        1682
```


```
TGGGCACTAA AAATTTGGTA ATGCTATACC AAAATATATA AAAAGATCTT        1732
```


```
GCTGGGTTTT GGTAAAAAAA AAAAAAAAAA A                            1763
```

3. DNA sequence with the coding region for sucrose
    phosphate - synthase for the preparation of sugar
    beet with changed sucrose concentration,
    characterised in that the sequence has the following
5   nucleotide sequence (Seq. ID No.3):

```
GGGCTGCAGG GAAGCTCTGA ACTTCAAAA ATG GCG GGA AAT GAT        0044
                                   Met Ala Gly Asn Asp
                                                   5
```


```
TGG ATA AAC AGT TAT TTA GAG GCA ATT CTG GAT GTG GGT CCA GGA  0089
Trp Ile Asn Ser Tyr Leu Glu Ala Ile Leu Asp Val Gly Pro Gly
                10              15                  20
```


```
CTT GAT GAT GCA AAA TCA TCT TTG CTT TTG AGA GAA AGA GGC AGG  0134
Leu Asp Asp Ala Lys Ser Ser Leu Leu Leu Arg Glu Arg Gly Arg
                25              30                  35
```

55

```
TTT AGT CCT ACT CGT TAC TTT GTT GAA GAA GTT ATC ACT GGT TTT   0179
Phe Ser Pro Thr Arg Tyr Phe Val Glu Glu Val Ile Thr Gly Phe
            40                  45                  50


GAT GAA ACC GAC CTT CAT CGT TCA TGG GTT CGG GCA CAA GCA ACA   0224
Asp Glu Thr Asp Leu His Arg Ser Trp Val Arg Ala Gln Ala Thr
            55                  60                  65


AGG AGT CCT CAA GAG AGG AAT ACT AGA TTG GAG AAC ATG TGT TGG   0269
Arg Ser Pro Gln Glu Arg Asn Thr Arg Leu Glu Asn Met Cys Trp
            70                  75                  80


AGA ATT TGG AAT TTG GCT CGT CAG AAG AAG CAG CTT GAG AAT GAA   0314
Arg Ile Trp Asn Leu Ala Arg Gln Lys Lys Gln Leu Glu Asn Glu
            85                  90                  95


GAA GCT CAG CGG AAG ACA AAA CGT CGT ATG GAG CTT GAG AGG GGT   0359
Glu Ala Gln Arg Lys Thr Lys Arg Arg Met Glu Leu Glu Arg Gly
            100                 105                 110


CGT CGA GAA GCA ACT GCT GAT ATG TCG GAG GAC TTA TCA GAA GGC   0404
Arg Arg Glu Ala Thr Ala Asp Met Ser Glu Asp Leu Ser Glu Gly
            115                 120                 125


GAA AAG GAC ATT TCA GCT CAT GGT GAT AGC ACC CGT CCT AGA TTG   0449
Glu Lys Asp Ile Ser Ala His Gly Asp Ser Thr Arg Pro Arg Leu
            130                 135                 140


CCA AGA ATA AAT TCT CTT GAT GCT ATG GAG ACA TGG ATT AGT CAA   0494
Pro Arg Ile Asn Ser Leu Asp Ala Met Glu Thr Trp Ile Ser Gln
            145                 150                 155
```

56

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CAA AAG GAA AAA AAA CTC TAC CTT GTT TTG ATA AGT CTT CAT GGT   0539
Gln Lys Glu Lys Lys Leu Tyr Leu Val Leu Ile Ser Leu His Gly
            160             165             170


TTG ATA CGA GGT GAA AAC ATG GAA CTT GGC CGT GAT TCT GAT ACT   0584
Leu Ile Arg Gly Glu Asn Met Glu Leu Gly Arg Asp Ser Asp Thr
            175             180             185


GGT GGT CAG GTT AAG TAT GTG GTT GAG CTT GCA AGG GCT CTA GGT   0629
Gly Gly Gln Val Lys Tyr Val Val Glu Leu Ala Arg Ala Leu Gly
            190             195             200


TCG ATG CCA GGT GTT TAT AGA GTT GAT TTG CTA ACT AGG CAA GTT   0674
Ser Met Pro Gly Val Tyr Arg Val Asp Leu Leu Thr Arg Gln Val
            205             210             215


TCA TCT CCT GAC GTG GAT TGG AGT TAT GGG GAG CCT ACT GAG ATG   0719
Ser Ser Pro Asp Val Asp Trp Ser Tyr Gly Glu Pro Thr Glu Met
            220             225             230


CTG AAT CCA AGG GAT TCC AAT GGT TTT GAT GAT GAT GAT GAT GAA   0764
Leu Asn Pro Arg Asp Ser Asn Gly Phe Asp Asp Asp Asp Asp Glu
            235             240             245


ATG GGA GAG AGT AGT GGT GCT TAC ATT GTT CGT ATA CCA TTT GGG   0809
Met Gly Glu Ser Ser Gly Ala Tyr Ile Val Arg Ile Pro Phe Gly
            250             255             260
```

57

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CCG AGG GAT AAG TAT ATC GCA AAA GAA GAG CTT TGG CCC TAT ATT    0854
Pro Arg Asp Lys Tyr Ile Ala Lys Glu Glu Leu Trp Pro Tyr Ile
            265                 270                 275


CCT GAA TTT GTT GAT GGT GCT CTA AAC CAC ATA GTT CAA ATG TCC    0899
Pro Glu Phe Val Asp Gly Ala Leu Asn His Ile Val Gln Met Ser
            280                 285                 290


AAA GTT TTA GGT GAG CAA ATT GGT AGC GGG GAA ACA GTT TGG CCA    0944
Lys Val Leu Gly Glu Gln Ile Gly Ser Gly Glu Thr Val Trp Pro
            295                 300                 305


GTT GCC ATT CAT GGA CAT TAT GCT GAT GCT GGT GAT TCT GCT GCT    0989
Val Ala Ile His Gly His Tyr Ala Asp Ala Gly Asp Ser Ala Ala
            310                 315                 320


CTT CTT TCT GGT GGC CTA AAT GTT CCA ATG CTT TTA ACG GGG CAT    1034
Leu Leu Ser Gly Gly Leu Asn Val Pro Met Leu Leu Thr Gly His
            325                 330                 335


TCT CTT GGC CGA GAC AAG TTA GAG CAG CTC CTC AAA CAG GGT CGA    1079
Ser Leu Gly Arg Asp Lys Leu Glu Gln Leu Leu Lys Gln Gly Arg
            340                 345                 350


ATG TCT AAA GAT GAC ATA AAC AAT ACA TAC AAA ATA ATG CGT AGG    1124
Met Ser Lys Asp Asp Ile Asn Asn Thr Tyr Lys Ile Met Arg Arg
            355                 360                 365
```

58

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ATA GAA GCC GAA GAG TTA TCA CTT GAT GCC TCT GAG ATA GTC ATA    1169
Ile Glu Ala Glu Glu Leu Ser Leu Asp Ala Ser Glu Ile Val Ile
            370                 375                 380


ACT AGT ACA AGA CAA GAA ATA GAA GAG CAA TGG CAC CTC TAT GAT    1214
Thr Ser Thr Arg Gln Glu Ile Glu Glu Gln Trp His Leu Tyr Asp
            385                 390                 395


GGG TTT GAT CCT GTG CTA GAA CGT AAA CTC CGT GCT AGG ATG AAG    1259
Gly Phe Asp Pro Val Leu Glu Arg Lys Leu Arg Ala Arg Met Lys
            400                 405                 410


CGT GGT GTA AGC TGT TAT GGA AGG TTC ATG CCC CGG ATG GTT GTT    1304
Arg Gly Val Ser Cys Tyr Gly Arg Phe Met Pro Arg Met Val Val
            415                 420                 425


ATT CCT CCT GGA ATG GAA TTC AAT CAT ATT GTT CCA CAT GAG GGT    1349
Ile Pro Pro Gly Met Glu Phe Asn His Ile Val Pro His Glu Gly
            430                 435                 440


GAT ATG GAT GGT GAA ACA GAA GAA ACT GAA GAG CAT CCT ACA TCA    1394
Asp Met Asp Gly Glu Thr Glu Glu Thr Glu Glu His Pro Thr Ser
            445                 450                 455


CCT GAT CCA CCT ATC TGG GCT GAG ATT ATG CGC TTC TTT TCT AAA    1439
Pro Asp Pro Pro Ile Trp Ala Glu Ile Met Arg Phe Phe Ser Lys
            460                 465                 470
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59

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CCA AGG AAG CCA ATG ATA CTT GCC CTT GCT AGG CCT GAC CCG AAG   1484
Pro Arg Lys Pro Met Ile Leu Ala Leu Ala Arg Pro Asp Pro Lys
            475                 480                 485


AAG AAT ATC ACG ACT TTG GTC AAA GCA TTT GGA GAA TGC CGT CCA   1529
Lys Asn Ile Thr Thr Leu Val Lys Ala Phe Gly Glu Cys Arg Pro
            490                 495                 500


CTA AGG GAG CTA GCT AAT CTT ACT CTT ATA ATG GGT AAC CGA GAT   1574
Leu Arg Glu Leu Ala Asn Leu Thr Leu Ile Met Gly Asn Arg Asp
            505                 510                 515


GGT ATT GAC GAG ATG TCA AGC ACC AGT TCT TCA GTT CTC CTG TCA   1619
Gly Ile Asp Glu Met Ser Ser Thr Ser Ser Ser Val Leu Leu Ser
            520                 525                 530


GTG CTT AAG CTA ATT GAT CAA TAC GAC CTT TAT GGT CAA GTA GCA   1664
Val Leu Lys Leu Ile Asp Gln Tyr Asp Leu Tyr Gly Gln Val Ala
            535                 540                 545


TAC CCC AAA CAT CAC AAG CAA GCT GAT GTT CCT GAG ATT TAT CGT   1709
Tyr Pro Lys His His Lys Gln Ala Asp Val Pro Glu Ile Tyr Arg
            550                 555                 600


TTG GCA GCA AAG ACA AAG GGA GTC TTT ATT AAT CCA GCT TTT ATT   1754
Leu Ala Ala Lys Thr Lys Gly Val Phe Ile Asn Pro Ala Phe Ile
            605                 610                 615
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60

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GAG CCA TTT GGG CTG ACT CTA ATA GAG GCA GCA GCT CAT GGT TTA    1799
Glu Pro Phe Gly Leu Thr Leu Ile Glu Ala Ala Ala His Gly Leu
            620             625             630


CCG ATG GTT GCT ACG AAA AAT GGA GGC CCT GTT GAT ATC CAG AGG    1844
Pro Met Val Ala Thr Lys Asn Gly Gly Pro Val Asp Ile Gln Arg
            635             640             645


GTC CTT GAT AAT GGT CTT CTT GTG GAT CCT CAT GAG CAG CAG TCT    1889
Val Leu Asp Asn Gly Leu Leu Val Asp Pro His Glu Gln Gln Ser
            650             655             660


ATT GCT ACT GCT TTG CTG AAG CTT GTT GCT GAT AAG CAA CTA TGG    1934
Ile Ala Thr Ala Leu Leu Lys Leu Val Ala Asp Lys Gln Leu Trp
            665             670             675


ACA AAA TGC CAG CAA AAT GGA CTG AAA AAT ATT CAT CTC TAC TCT    1979
Thr Lys Cys Gln Gln Asn Gly Leu Lys Asn Ile His Leu Tyr Ser
            680             685             690


TGG CCA GAG CAT TCG AAG ACA TAC CTA TCT CGA ATA GCC AGT TCG    2024
Trp Pro Glu His Ser Lys Thr Tyr Leu Ser Arg Ile Ala Ser Ser
            695             700             705


AGA CAA AGG CAA CCA CAG TGG CAA AGA AGT AGT GAT GAA GGG CTT    2069
Arg Gln Arg Gln Pro Gln Trp Gln Arg Ser Ser Asp Glu Gly Leu
            710             715             720
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61

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GAC AAT CAA GAG CCT GAA TCT CCA AGT GAT TCT TTA AGA GAT ATA   2114
Asp Asn Gln Glu Pro Glu Ser Pro Ser Asp Ser Leu Arg Asp Ile
            725                 730                 735


AAG GAT ATA TCT CTA AAC CTT GAA GTT CTC GTT AGA CCG GAG AAA   2159
Lys Asp Ile Ser Leu Asn Leu Glu Val Leu Val Arg Pro Glu Lys
            740                 745                 750


AGG GTG AAG ACG TTG AAA ATC TTG GGA TTG ATG ACA AAA GCA AAT   2204
Arg Val Lys Thr Leu Lys Ile Leu Gly Leu Met Thr Lys Ala Asn
            755                 760                 765


TCG AGA ATG CTG TTA TGT TCA TGG TCT AAT GGT GTC CAT AAG ATG   2249
Ser Arg Met Leu Leu Cys Ser Trp Ser Asn Gly Val His Lys Met
            770                 775                 780


CTT CGG AAG GCT CGG TTC TCT GAC AAA GTA GAT CAG GCT TCT AGT   2294
Leu Arg Lys Ala Arg Phe Ser Asp Lys Val Asp Gln Ala Ser Ser
            785                 790                 795


AAA TAT CCA GCA TTT AGG AGG AGA AAA CTT ATA TAT GTT ATT GCT   2339
Lys Tyr Pro Ala Phe Arg Arg Arg Lys Leu Ile Tyr Val Ile Ala
            800                 805                 810


GTA GAC GGG GAT TAT GAA GAT GGA CTT TTT GAT ATT GTT CGG AGG   2384
Val Asp Gly Asp Tyr Glu Asp Gly Leu Phe Asp Ile Val Arg Arg
            815                 820                 825
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62

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ATA TTT GAT GCT GCT GGC AAG GAG AAG ATT GAA GGT TCC ATC GGG    2429
Ile Phe Asp Ala Ala Gly Lys Glu Lys Ile Glu Gly Ser Ile Gly
            830                 835                 840


TTT ATA TTG TCA ACA TCC TAT TCT ATG CCC GAA ATT CAG AAC TAT    2474
Phe Ile Leu Ser Thr Ser Tyr Ser Met Pro Glu Ile Gln Asn Tyr
            845                 850                 855


TTG CTA TCA AAA GGC TTC AAT CTT CAT GAT TTT GAT GCA TAT ATA    2519
Leu Leu Ser Lys Gly Phe Asn Leu His Asp Phe Asp Ala Tyr Ile
            860                 865                 870


TGC AAC AGT GGG AGT GAG TTG TAC TAT TCA TCT TTG AAC TCA GAG    2564
Cys Asn Ser Gly Ser Glu Leu Tyr Tyr Ser Ser Leu Asn Ser Glu
            875                 880                 885


GAG AGT AAT ATT ATA GCA GAT TCA GAT TAC CAT TCA CAC ATA GAG    2609
Glu Ser Asn Ile Ile Ala Asp Ser Asp Tyr His Ser His Ile Glu
            890                 895                 900


TAC AGA TGG GGT GGA GAA GGC CTT AGA AGG ACT TTG CTT CGC TGG    2654
Tyr Arg Trp Gly Gly Glu Gly Leu Arg Arg Thr Leu Leu Arg Trp
            905                 910                 915


GCA GCT TCC ATC ACA GAA AAA AAT GGT GAA AAC GAA GAA CAG GTT    2699
Ala Ala Ser Ile Thr Glu Lys Asn Gly Glu Asn Glu Glu Gln Val
            920                 925                 930
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63

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ATT ACT GAA GAT GAA GAA GTT TCT ACG GGT TAT TGC TTT GCG TTT   2744
Ile Thr Glu Asp Glu Glu Val Ser Thr Gly Tyr Cys Phe Ala Phe
            935             940             945


AAA ATA AAG AAC CAA AAT AAG GTT CCC CCT ACG AAG GAG CTC CGC   2789
Lys Ile Lys Asn Gln Asn Lys Val Pro Pro Thr Lys Glu Leu Arg
            950             955             960


AAG TCA ATG AGG ATT CAA GCT CTT CGT TGC CAT GTG ATT TAC TGT   2834
Lys Ser Met Arg Ile Gln Ala Leu Arg Cys His Val Ile Tyr Cys
            965             970             975


CAG AAC GGA TCT AAA ATG AAT GTG ATT CCA GTA CTA GCA TCC CGT   2879
Gln Asn Gly Ser Lys Met Asn Val Ile Pro Val Leu Ala Ser Arg
            980             985             990


TCT CAA GCC CTC AGG TAT CTT TAT GTT CGT TGG GGA GTT GAG TTG   2924
Ser Gln Ala Leu Arg Tyr Leu Tyr Val Arg Trp Gly Val Glu Leu
            995             1000            1005


TCG AAG ATG GTT GTC TTT GTT GGA GAA TGT GGT GAC ACA GAT TAT   2969
Ser Lys Met Val Val Phe Val Gly Glu Cys Gly Asp Thr Asp Tyr
            1010            1015            1020


GAA GGC TTG CTT GGC GGG GTC CAT AAA ACC GTA ATA CTG AAG GGA   3014
Glu Gly Leu Leu Gly Gly Val His Lys Thr Val Ile Leu Lys Gly
            1025            1030            1035
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64

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GTC TCC AAC ACT GCT TTA AGG TCT CTC CAT GCC AAC AGA AGT TAC    3059
Val Ser Asn Thr Ala Leu Arg Ser Leu His Ala Asn Arg Ser Tyr
        1040            1045                1050


CCT CTT TCA CAT GTC GTG TCG CTT GAC AGC CCC AAT ATT GGC GAG    3104
Pro Leu Ser His Val Val Ser Leu Asp Ser Pro Asn Ile Gly Glu
        1055            1060                1065


GTG AGC AAA GGG TGC AGC AGC TCC GAG ATC CAG TCC ATC GTC ACA    3149
Val Ser Lys Gly Cys Ser Ser Ser Glu Ile Gln Ser Ile Val Thr
        1070            1075                1080


AAA CTC TCC AAA GCT TAA TCAGATATCT GCTGCTTTCT TTTGGGTAAG       3197
Lys Leu Ser Lys Ala End
        1085
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CAAGGTTTCA TCTTATATGA TTATATCATA AGATACTATA TAAGCACCTT         3247

ATTGGTAAGT CAGTCCCATA ATAATAATGT ACTTCAGAAC CACAATACTT         3297

AAAAGTTGGT TCAGTAGTGA TTAGTCTCAT AATAATCATA TAATTACACA         3347

TCCGCTGTTA ACTAGTGGTA ATATCTAAGC TCAACAATAA AGATGTAAAA         3397

TGCTAGTATG GAAATGAATT GCTAGCTGTT GATCTCTTTC CCTTTATTCT         3447

GTATTATTTC TTTCCTCATC TCATGTAAAA ACAATTTTCT GAAGGTGTAC         3497

AGTTTTTTCC CCTTATATAT CTGTATTATT TCTACTATTT TTTGTTTGTA         3547

AGAATATCCT CTCATCGAGG AGTGATAATT AAATAACCGG CTTGCTAAAT         3597
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65

ATAAAGCTTA TTCGAGTTAA AAAAAAAAAA AAAAAAA   3635

     4.   DNA sequence with the coding region for
           sucrose-synthase for the preparation of sugar beet
           with modified sucrose concentration, characterised
           in that the sequence has the following nucleotide
     5   sequence (Seq. ID No.4):

   CT GCA GGA GGG AAA CAA ATT CTT AGC GAT GGC CCG TTT AGC GAA   0044
      Ala Gly Gly Lys Gln Ile Leu Ser Asp Gly Pro Phe Ser Glu
                         5   10

   GTT CTT AGG TCT GCT CAG GAA GCA ATA GTT GTT CCT CCC TTT GTT   0089
   Val Leu Arg Ser Ala Gln Glu Ala Ile Val Val Pro Pro Phe Val
   15   20   25

   GCT ATA GCA GTC CGT CCA AGA CCT GGA GTT TGG GAA TAT GTT CGT   0134
   Ala Ile Ala Val Arg Pro Arg Pro Gly Val Trp Glu Tyr Val Arg
   30   35   40

   GTT AAT GTC TCT GAA CTG AAT GTG GAG CAG CTA ACT GTG TCT GAG   0179
   Val Asn Val Ser Glu Leu Asn Val Glu Gln Leu Thr Val Ser Glu
   45   50   55

   TAT CTC CAT TTC AAG GAA GAA CTT GTG GAT GGA AAG GCT GAT GAC   0224
   Tyr Leu His Phe Lys Glu Glu Leu Val Asp Gly Lys Ala Asp Asp
   60   65   70

   CAC TAT GTG CTT GAG CTT GAT TTC GAG CCT TTT AAT GAA TCA GTT   0269
   His Tyr Val Leu Glu Leu Asp Phe Glu Pro Phe Asn Glu Ser Val
   75   80   85

   CCA CGT CCA ACT CGC TCT TCA TCA ATT GGT AAT GGT GTT CAG TTC   0314
   Pro Arg Pro Thr Arg Ser Ser Ser Ile Gly Asn Gly Val Gln Phe
   90   95   100

66

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CTC AAT CGG CAC CTG TCA TCA AGC ATG TTC TGC AAC AAA GAT TGC      0359
Leu Asn Arg His Leu Ser Ser Ser Met Phe Cys Asn Lys Asp Cys
105             110             115


TTG GAG CCG TTA CTT GAT TTT CTT AGA GTG CAC AAA CAT AAA GGA      0404
Leu Glu Pro Leu Leu Asp Phe Leu Arg Val His Lys His Lys Gly
120             125             130


GTT GTC ATG ATG TTG AAT GAT CGG ATA CAG ACT ATC CAG CGT CTT      0449
Val Val Met Met Leu Asn Asp Arg Ile Gln Thr Ile Gln Arg Leu
135             140             145


CAG TCT GCA TTG TCT AAA GCT GAG GAT TAT CTT ATC AAA CTT CCA      0494
Gln Ser Ala Leu Ser Lys Ala Glu Asp Tyr Leu Ile Lys Leu Pro
150             155             160


GCA GAT ACA CCT TAC TCT GAG TTC GAA TTT GTA ATC CAA GGT ATG      0539
Ala Asp Thr Pro Tyr Ser Glu Phe Glu Phe Val Ile Gln Gly Met
165             170             175


GGT TTT GAA AGA GGC TGG GGT GAT ACT GCT GAA AGG GTT CTA GAA      0584
Gly Phe Glu Arg Gly Trp Gly Asp Thr Ala Glu Arg Val Leu Glu
180             185             190


ATG ATG CAT CTA CTA CTA GAT ATC CTT CAG GCT CCC GAT CCG TCT      0629
Met Met His Leu Leu Leu Asp Ile Leu Gln Ala Pro Asp Pro Ser
195             200             205
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67

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ACA TTA GAG ACA TTT CTG GGA AGA CTT CCC ATG GTG TTT AAT GTG    0674
Thr Leu Glu Thr Phe Leu Gly Arg Leu Pro Met Val Phe Asn Val
210                 215                 220


GTC ATT TTG TCT GTA CAT GGA TAT TTT GGA CAG GCA CAT GTG CTC    0719
Val Ile Leu Ser Val His Gly Tyr Phe Gly Gln Ala His Val Leu
225                 230                 235


GGC TTG CCT GAC ACT GGT GGG CAG ATA GTT TAT ATA CTT GAC CAA    0764
Gly Leu Pro Asp Thr Gly Gly Gln Ile Val Tyr Ile Leu Asp Gln
240                 245                 250


GTG CGG TCT CTG GAA CAT GAA ATG CTC CAA CGA ATA AAG AAG CAA    0809
Val Arg Ser Leu Glu His Glu Met Leu Gln Arg Ile Lys Lys Gln
255                 260                 265


GGA CTA GAT GTG ACT CCT AGA ATT CTT ATC GTG AGT CGG TTG ATT    0854
Gly Leu Asp Val Thr Pro Arg Ile Leu Ile Val Ser Arg Leu Ile
270                 275                 280


CCT GAC GCT AAA GGG ACC ACG TGC AAT CAA CGT ATG GAG AAA GTC    0899
Pro Asp Ala Lys Gly Thr Thr Cys Asn Gln Arg Met Glu Lys Val
285                 290                 295


AGT GGA ACA GAG CAT GCT AGT ATC CTG AGA GTT CCT TTC CGA TCA    0944
Ser Gly Thr Glu His Ala Ser Ile Leu Arg Val Pro Phe Arg Ser
300                 305                 310
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68

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GAG AAA GGA ATC CTC CGC AAA TGG ATA TCT AGA TTT GAT GTA TGG      0989
Glu Lys Gly Ile Leu Arg Lys Trp Ile Ser Arg Phe Asp Val Trp
315                 320             325


CCT TAT TTA GAG ACC TTC ACT GAG GAT GCA GCT GGT GAA ATT ATT      1034
Pro Tyr Leu Glu Thr Phe Thr Glu Asp Ala Ala Gly Glu Ile Ile
330                 335             340


GGC GAG TTG CAG GGT CGT CCA GAT CTG ATA ATT GGC AAC TAC AGC      1079
Gly Glu Leu Gln Gly Arg Pro Asp Leu Ile Ile Gly Asn Tyr Ser
345                 350             355


GAT GGG AAT ATA GTT GCT TCT TTA TTG TCC CAC AAA ATG GGT GTC      1124
Asp Gly Asn Ile Val Ala Ser Leu Leu Ser His Lys Met Gly Val
360                 365             370


ACC CAG TGC AAT ATA GCC CAT GCA TTG GAG AAA ACC AAG TAT CCA      1169
Thr Gln Cys Asn Ile Ala His Ala Leu Glu Lys Thr Lys Tyr Pro
375                 380             385


GAT TCT GAT ATT TAC TGG AAA AGA TTT GAG GAC AAA TAT CAC TTC      1214
Asp Ser Asp Ile Tyr Trp Lys Arg Phe Glu Asp Lys Tyr His Phe
390                 395             400


TCG TGT CAA TTT TCA GCT GAC TTG ATG GCA ATG AAT CAT GCT GAT      1259
Ser Cys Gln Phe Ser Ala Asp Leu Met Ala Met Asn His Ala Asp
405                 410             415
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69

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TTC ATC ATT ACG AGT ACT TAC CAA GAG ATA GCT GGA ACG AAG AAT    1304
Phe Ile Ile Thr Ser Thr Tyr Gln Glu Ile Ala Gly Thr Lys Asn
420             425             430


ACT GTT GGT CAA TAT GAA AGC CAT AAG GCC TTT ACT TTT CCG GGG    1349
Thr Val Gly Gln Tyr Glu Ser His Lys Ala Phe Thr Phe Pro Gly
435             440             445


CTG TAT CGG GTG GTT CAC GGG ATT GAT GTC TTT GAT CCC AAG TTT    1394
Leu Tyr Arg Val Val His Gly Ile Asp Val Phe Asp Pro Lys Phe
450             455             460


AAT ATT GTC TCG CCA GGG GCA GAC ATG GCC ATC TAC TTC CCA TTT    1439
Asn Ile Val Ser Pro Gly Ala Asp Met Ala Ile Tyr Phe Pro Phe
465             470             475


TCA GAG AAG GAT GTC ACC TGT CTC ACT TCA CTT CAT AGA CTT ATA    1484
Ser Glu Lys Asp Val Thr Cys Leu Thr Ser Leu His Arg Leu Ile
480             485             490


GAG CAG CTC CTA TTC AAA CCT GAG CAG AAC GAA GAA CAC ATT GGT    1529
Glu Gln Leu Leu Phe Lys Pro Glu Gln Asn Glu Glu His Ile Gly
495             500             505 .


GTA TTA GAT GAT ACC TCA AAG CCA ATT ATA TTT TCC ATG GCG AGG    1574
Val Leu Asp Asp Thr Ser Lys Pro Ile Ile Phe Ser Met Ala Arg
510             515             520
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70

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CTA GAC CGT GTG AAG AAT ATA ACA GGG CTG GTA GAG TGC TAT GGC          1619
Leu Asp Arg Val Lys Asn Ile Thr Gly Leu Val Glu Cys Tyr Gly
525                 530                 535


AAG AAT GCG AAA CTC AGG GAA CTG GCA AAC CTG GTT GTA GTG GCT          1664
Lys Asn Ala Lys Leu Arg Glu Leu Ala Asn Leu Val Val Val Ala
540                 545                 550


GGG TAC AAT GAT GTA AAA AAG TCG AAT GAC AGG GAG GAA ATT GCC          1709
Gly Tyr Asn Asp Val Lys Lys Ser Asn Asp Arg Glu Glu Ile Ala
555                 560                 565


GAA ATC GAG AAG ATG CAC AGG CTT ATA CAG GAG TAT AAT TTA AGA          1754
Glu Ile Glu Lys Met His Arg Leu Ile Gln Glu Tyr Asn Leu Arg
570                 575                 580


GGA CAA TTT CGC TGG ATT GCT TCT CAA ACA AAT AGA GTA CGA AAT          1799
Gly Gln Phe Arg Trp Ile Ala Ser Gln Thr Asn Arg Val Arg Asn
585                 590                 595


GGT GAA CTC TAT CGC TAC ATT TGT GAC AAA GGA GGT ATT TTT GCG          1844
Gly Glu Leu Tyr Arg Tyr Ile Cys Asp Lys Gly Gly Ile Phe Ala
600                 605                 610


CAG CCT GCA TTT TAT GAA GCA TTT GGG CTT ACA GTT GTT GAA GCC          1889
Gln Pro Ala Phe Tyr Glu Ala Phe Gly Leu Thr Val Val Glu Ala
615                 620                 625
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71

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ATG ACC TGT GGT CTT CCC ACA TTT GCT ACC TGC CAC GGT GGT CCA        1934
Met Thr Cys Gly Leu Pro Thr Phe Ala Thr Cys His Gly Gly Pro
630             635             640


GCT GAG ATT ATA GAA GAC GGT GTT TCA GGA TTT CAT ATC GAT CCA        1979
Ala Glu Ile Ile Glu Asp Gly Val Ser Gly Phe His Ile Asp Pro
645             650             655


TAT CAT GCT GAT CAG GCA GAA AAA ATG ACT GAA TTC TTT GTC AAG        2024
Tyr His Ala Asp Gln Ala Glu Lys Met Thr Glu Phe Phe Val Lys
660             665             670


TGC AGA GAG GAT CCA AAC TAC TGG ACT AAA ATC TCT GCA GGA GGG        2069
Cys Arg Glu Asp Pro Asn Tyr Trp Thr Lys Ile Ser Ala Gly Gly
675             680             685


TTA CTA AGG ATC AAA GAA AGA TAT ACC TGG CAA AAG TAT TCT GAA        2114
Leu Leu Arg Ile Lys Glu Arg Tyr Thr Trp Gln Lys Tyr Ser Glu
690             695             700


AGG TTA ATG ACA TTG GCA GGG GTG TAT GGT TTC TGG AAA TAT GTC        2159
Arg Leu Met Thr Leu Ala Gly Val Tyr Gly Phe Trp Lys Tyr Val
705             710             715


TCT AAA CTA GAG AGA AGA GAG ACA CGA CGT TAT CTT GAG ATG TTC        2204
Ser Lys Leu Glu Arg Arg Glu Thr Arg Arg Tyr Leu Glu Met Phe
720             725             730
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TAC ATT TTG AAG TTC CGT GAT CTG GCC AAC TCT GTT CCG CTG GCA    2249
Tyr Ile Leu Lys Phe Arg Asp Leu Ala Asn Ser Val Pro Leu Ala
735             740             745


ACA GAT GAA GAG CCT TCT ACT ACT GAT GCA GTT GCG ACA TTC CGT    2294
Thr Asp Glu Glu Pro Ser Thr Thr Asp Ala Val Ala Thr Phe Arg
750             755             760


GGA CCT TGA ACGCTGCTGC TTACTGAGGT TCCAAGTTGT GTATATATTA        2343
Gly Pro End


CTGTGAAAGG AATAAGTGTA GCTACACAAA AGGTTCTCAA CTATTAGTAT         2393

CTTCTCTGTG TAAATAACGA GAGTGAAAAA TGTAATATTG TTGATGTCTT         2443

GAAAACTGAG TTTGCTTTGT TTATTTTTAA GTGTATGACA ATATGTATCA         2493

TATAACGGAT TCTTCAGTGA TCATATCAAA AACTACTGAC CATCGAAGTT         2543

AATGAAAATC GACAGCAACA                                           2563
```

5.   Derivatives of DNA sequences according to any one of
      claims 1 to 4 characterised in that these
      derivatives are obtained by exchange of single bases
5   or by targeted or non-targeted mutagenesis.

6.   Plasmids containing
      a)   a suitable promoter which ensures that the
            coding sequence meets a suitable time point or
10   in the specified developments in the transgenic
            plant or in determined genes of transgenic
            plants;

73

b)   at least one coding sequence according to
     claims 1 to 5, that
     i)   is so coupled to the promoter that the
           formation of an RNA is allowed which is
           into a protein, whereby the protein
           demonstrates an enzymatic activity which
           leads to a modification of the sucrose
           concentration in the plant, or
     ii)   which is so coupled to the promoter that
           the coding part is read, which leads to
           the formation of a so-called anti-sense
           RNA which under-expresses the formation
           of the protein coded from an endogenous
           gene in the plant, that is involved in
           the sucrose biosynthesis; and

c)   A non-coding termination sequence that contains
     the signal for the termination and poly-
     adenylation of the transcript.

7.   Use of the DNA-sequences according to any one of
     claims 1 to 6 for the preparation of sugar beet with
     changed sucrose concentration.

8.   Use of the plasmids according to any one of claims
     1-4 for the preparation of derivatives by targeted
     or non-targeted mutagenesis

9.   Sugar beet containing a DNA sequence according to
     any one of claims 1-5.